

GenCore version 5.1.4_p5_4578
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OM nucleotide - nucleotide search, using sw model

Run on: March 17, 2003, 18:53:06 : Search time 1474 Seconds
(without alignments)
2593.036 Million cell updates/sec

Title: US-09-247-874C-2_COPY_8710_8945

Perfect score: 236
Sequence: 1 ttgtgcatctggtcattat.....ataactcactgaataaaa 236

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum hit seq length: 0
Maximum hit seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: *
1: em_estdb: *
2: em_estdb: *
3: em_estdb: *
4: em_estdb: *
5: em_estdb: *
6: em_estdb: *
7: em_estdb: *
8: em_estdb: *
9: em_estdb: *
10: em_estdb: *
11: em_estdb: *
12: em_estdb: *
13: em_estdb: *
14: em_estdb: *
15: em_estdb: *
16: em_estdb: *
17: em_estdb: *
18: em_estdb: *
19: em_estdb: *
20: em_estdb: *
21: em_estdb: *
22: em_estdb: *
23: em_estdb: *
24: em_estdb: *
25: em_estdb: *
26: em_estdb: *
27: em_estdb: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB	ID	Description
1	231.8	98.2	413	14	W38319	W38319.rc77b02.s1
2	231.8	98.2	514	9	AA131744	AA131744.z135102.s
3	231.8	98.2	554	9	AA577318	AA577318.nm9a08.s
4	231.8	98.2	703	14	BO001221	BO001221.U1-H-DH1-
5	231.8	98.2	770	14	BO000281	BO000281.U1-H-DP0-
6	229.8	97.4	429	14	T29172	T29172.FST71708.HD

7	228.6	96.9	375	12	B019263	B019263
8	228.6	96.7	548	14	BM992737	BM992737.U1-H-DH0-
9	228.2	96.5	698	9	AT471571	AT471571
10	227.8	96.5	424	9	AA923615	AA923615
11	227.8	96.5	528	9	AT678441	AT678441.U082401.x
12	227.2	96.3	549	9	AT566941	AT566941.LG67B02.x
13	227	96.2	521	9	AT022464	AT022464.ow64405.x
14	226.8	96.1	314	9	AA382165	AA382165.EST195428
15	226.2	95.8	618	10	AA273081	AA273081.x027b01.x
16	225.2	95.4	415	9	AA362146	AA362146.EST171810
17	223.5	94.7	817	9	AT609005	AT609005.TW85907.x
18	217.8	92.3	430	14	WA7101	WA7101.zc39b04.s1
19	217.8	92.3	793	14	BM999417	BM999417.U1-H-DH0-
20	216.2	91.6	911	12	B0194765	B0194765.EST14064
21	209.6	88.8	223	9	AA362379	AA362379.EST171816
22	195	82.6	454	14	D20737	D20737.HMG501714
23	193.4	81.9	196	9	AA362067	AA362067.EST171531
24	186.2	78.9	749	12	B0117168	B0117168.60244445
25	179	75.8	286	10	B0183186	B0183186.RC4.H1065
26	164.4	69.7	252	10	AA779422	AA779422.bv4a09.x
27	156.6	66.4	241	14	C06317	C06317.C06317.Hma
28	149.4	63.3	746	13	B1519707	B1519707.603051928
29	146.2	61.9	925	10	B0119601	B0119601.601472701
30	131.8	55.8	619	10	AA954756	AA954756.EST165826
31	118	50.0	325	14	BM734809	BM734809.M0N01.15
32	118	50.0	325	14	BM734809	BM734809.M0N01.15
33	118	50.0	355	14	BM734809	BM734809.M0N01.15
34	118	50.0	389	14	BM734809	BM734809.M0N01.15
35	118	50.0	638	14	BM734809	BM734809.M0N01.15
36	117	49.6	413	14	BM734809	BM734809.M0N01.15
37	114.4	48.5	565	13	B1961894	B1961894.M0N01.15
38	114.4	48.5	578	13	B1961894	B1961894.M0N01.15
39	114.4	48.5	689	13	B1961894	B1961894.M0N01.15
40	110.6	46.9	691	13	B1961894	B1961894.M0N01.15
41	101.4	43.0	342	14	B0600541	B0600541.M1-P-E7-a
42	101.4	43.0	508	14	B0600473	B0600473.M1-P-E7-a
43	99.8	42.3	343	14	B0600642	B0600642.M1-P-E7-a
44	99.8	42.3	372	14	B0600032	B0600032.M1-P-E7-a
45	99.8	42.3	474	14	B0600059	B0600059.M1-P-E7-a

ALIGNMENTS

RESULT 1
W38319 413 bp mRNA linear EST 15-MAY-1996
LOCUS zc77b02.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328299
DEFINITION similar to gb:M15310 INTERLORIN-1 BETA PROTECTOR (HUMAN); mRNA
SEQUENCE.
W38319 413 bp mRNA linear EST 15-MAY-1996
W38319 413 bp mRNA linear EST 15-MAY-1996
W38319 413 bp mRNA linear EST 15-MAY-1996

ACCESSION W38319
VERSION W38319.1 GI:119934
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens

REFERENCE
AUTHORS Chisoc, S., Dietrich, N., Becker, M., Bonaldi, M.F., Favetto, A., Gish, W., Hawkins, M., Hultman, M., Kucadze, T., Lacy, M., Le, M., Le, N., Matulis, E., Moore, J.B., Morris, M., Parsons, J., Prange, C., Riklin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierly-Mag, U., Trevisan, F., Underwood, K., Woldmann, P., Waterston, R., Wilson, R. and Merra M.
Generation and analysis of 280,000 human expressed sequence tags

TITLE JOURNAL MEDLINE
COMMENT 97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LNC: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mab-hema-ET
High quality sequence stop: 468.

FEATURES

Source

Location/Qualifiers

1..413

/organism "Homo sapiens"

/db_xref "GDB:1262503"

/db_xref "taxon:9606"

/clone "IMAGE:328299"

/clone_lib "Pancreatic Islet"

/tissue_type "pancreatic islet"

/lab_host "Sole cells (Kanamycin resistant)"

/note "Organ: Pancreas; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993)

Takada et al. cloned unidirectionally. Primer: 01490 dT.

5' adaptor sequence: 5' GAATGGGACGACG 3' -3' adaptor

sequence: 5' CCGACGTTTCTTTTCTTTT 3' "

BASE COUNT 155 a 65 c 86 g 127 t
ORIGIN

Query Match 98.2% Score 231.8; DB 14; Length 413;
Post Local Similarity 99.1%; Pred. No. 1.4e-48;
Matches 233; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 2 TTGATTCATTCGCTTATTATTTCAAGGGGCGAGACAGTGTCTCTTAAAGAG 61
DB 243 TTTATTCATTCGCTTATTATTTCAAGGGGCGAGAGAGAGTGTCTCTTAAAGAG 184
DB 62 CTTAGTTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 121
DB 184 CTTAGTTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 124
DB 122 AGTCTTTAAATTAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 181
DB 124 AGTCTTTAAATTAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 64
DB 182 AATGACCAAAATATATATCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 236
DB 64 AATGACCAAAATATATATCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 9

RESULT 2
AA131744/c 514 bp mRNA linear EST 27-Nov-1996
LOCUS
DEFINITION
IMAGE:503941.47 similar to db:M15340 INTERLEUKIN-1 BETA PRECURSOR (HUMAN); mRNA sequence.

ACCESSION
AA131744
VERSION
AA131744.1 GI:1694270
KEYWORDS
EST.

ORGANISM
human.

SOURCE
human.

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 514)

Hillier, D., Clark, M., Duboucq, T., Elliston, K., Hawkins, M., Holman

M., Bulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

Ricklin, D., Robinson, T., Soares, M., Tan, F., Trivaskis, E., Waterston

R., Williamson, A., Mohlmann, P., and Willson, R.

The Washington University Genome Sequencing Center

Washington University School of Medicine

4444 Forest Park Parkway, Box #501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: post@wustl.edu

This clone is available royalty-free through LNC: contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40813 fwd. from AmerSham

High quality sequence stop: 477.

Location/Qualifiers

Source

1..514

/organism "Homo sapiens"

/db_xref "GDB:3808919"

/db_xref "taxon:9606"

/clone "IMAGE:503941"

/clone_lib "Soares-Premature Interus_MH90"

/sex "female"

/dev_stage "adult"

/lab_host "BHL10"

/note "Organ: uterus; Vector: pTZ19; Site_1: Not 1;

Site_2: Eco RI; 1st strand cDNA was primed with a Not 1

oligo(dT) primer 15.

AATGACCAAAATATATATCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA

AGCTTAAATTAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA

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AGCTTAAATTAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA

Email: cgabs-rt@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINT at:
<http://image.llnl.gov>
 Plate: L1AM10219 row: q column: 10
 High quality sequence stop: 367.
 Location/Qualifiers
 1. 375
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NIH_MGC_90"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.7 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC library."

BASE COUNT 131 a 64 c 59 g 121 t
 ORIGIN

Query Match 96.9%; Score 228.6; DB 12; Length 375;
 Best Local Similarity 98.3%; Pred. No. 9.1e-48;
 Matches 231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTGATTCATTCGTCGTAATTATTCAGAGGGGCGCAGACGACGACGTCGTAAGAG 61
 DB 119 TTTTATTCATTCGTCGTAATTATTCAGAGGGGCGCAGACGACGTCGTAAGAG 178
 QY 62 CCTAGTTTAAAGCTATGGAATCAATTCATTTGGAGCTGCTGCTCTTTAATCA 121
 DB 179 CCTAGTTTAAAGCTATGGAATCAATTCATTTGGAGCTGCTGCTCTTTAATCA 238
 QY 122 AGTCCTTTAATTAAGCTAAATATTAAGCTACATTTAATATGGAATATTATA 181
 DB 239 AGTCCTTTAATTAAGCTAAATATTAAGCTACATTTAATATGGAATATTATA 298
 QY 182 AATGACCAATATGATACGTCGTAATGCTGCAATTAACCTCAGTGAAGAAA 236
 DB 299 AATGACCAATATGATACGTCGTAATGCTGCAATTAACCTCAGTGAAGAAA 353

RESULT 8
 BM997237 548 bp mRNA linear EST 17-JUN-2002
 LOCUS U1-H-DHO-aug-1-03-0-01.sl NC1_CGAP_DHO Homo sapiens cDNA clone
 IMAGE:5872130 4', mRNA sequence.
 ACCESSION BM997237
 VERSION BM997237.1 GI:19722138
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 548)
 NC1_CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

REFERENCE
 AUTHORS Contact: Robert Strausberg, Ph.D.
 TITLE Email: cgabs-rt@mail.nih.gov
 JOURNAL Tissue Procurement: Dr. Jose Morcneau
 COMMENT cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINT at: <http://image.llnl.gov>
 The following repetitive elements were found in this cDNA

sequence: 221-272, >(TAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA-Tes.
 Location/Qualifiers
 1. 548
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NC1_CGAP_DHO"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="organ: lung; Vector: p1773-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR 1; Site_2: Not 1;
 NC1_CGAP_DHO is a cDNA library containing the following
 tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma
 in lung. The library was constructed according to Bonaldi,
 Lennon and Soares, Genome Research, 6:791-806, 1996. First
 strand cDNA synthesis was primed with an oligo-dT primer
 containing a Not 1 site. Double stranded cDNA was ligated
 to an EcoR 1 adaptor, digested with Not 1, and cloned
 directionally into p1773-Pac vector. The oligonucleotide
 used to prime the synthesis of first strand cDNA contains
 a library tag sequence that is located between the Not 1
 site and the (dP)18 tail. The sequence tag for this
 library is AGATCATTCG.
 TAG_L1B-U1-H-DHO
 TAG_P1SSUE-lung
 TAG_SEU-ACATCATTCG"

BASE COUNT 172 a 95 c 123 g 158 t
 ORIGIN

Query Match 96.9%; Score 228.6; DB 14; Length 548;
 Best Local Similarity 98.3%; Pred. No. 9.4e-48;
 Matches 231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTGATTCATTCGTCGTAATTATTCAGAGGGGCGCAGACGACGTCGTAAGAG 61
 DB 246 TTTTATTCATTCGTCGTAATTATTCAGAGGGGCGCAGACGACGTCGTAAGAG 187
 QY 62 CCTAGTTTAAAGCTATGGAATCAATTCATTTGGAGCTGCTGCTCTTTAATCA 121
 DB 186 CCTAGTTTAAAGCTATGGAATCAATTCATTTGGAGCTGCTGCTCTTTAATCA 127
 QY 122 AGTCCTTTAATTAAGCTAAATATTAAGCTACATTTAATATGGAATATTATA 181
 DB 126 AGTCCTTTAATTAAGCTAAATATTAAGCTACATTTAATATGGAATATTATA 67
 QY 182 AATGACCAATATGATACGTCGTAATGCTGCAATTAACCTCAGTGAAGAAA 236
 DB 66 AATGACCAATATGATACGTCGTAATGCTGCAATTAACCTCAGTGAAGAAA 12

RESULT 9
 A1471571 698 bp mRNA linear EST 14-APR-1999
 LOCUS U198h09.x1 NC1_CGAP_C014 Homo sapiens cDNA clone IMAGE:215514 4'
 DEFINITION similar to gb:M15140 INTERLUKIN-1 BETA PRECURSOR (HUMAN); mRNA
 sequence.
 ACCESSION A1471571
 VERSION A1471571.1 GI:433661
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 698)
 NC1_CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

REFERENCE
 AUTHORS Contact: Robert Strausberg, Ph.D.
 TITLE Email: cgabs-rt@mail.nih.gov
 JOURNAL Tissue Procurement: Dr. Jose Morcneau
 COMMENT cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINT at: <http://image.llnl.gov>
 The following repetitive elements were found in this cDNA

Issue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CCAP clone distribution information can be found through the J.M.A.G.B. Consortium/ILNC at: www.bio.uth.tmc.edu/bhrp/imagc/imagc.html
 Insert Length: 1522 Std Error: 0.00
 Seq primer: 40bp from 5' end
 High quality sequence stop: 411.
 Location/Qualifiers

FEATURES

SOURCE

1..649
 /organism "Homo sapiens"
 /db_xref "taxon:9606"
 /clone "IMAGE:2155169"
 /clone_lib "NCI-CCAP COL4"
 /issue_type "moderately-differentiated adenocarcinoma"
 /lab_host "DH10B"
 /note "organ: colon; Vector: pCMV-Sport6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: 0140 dt. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"

BASE COUNT 206 a 141 c 161 g 187 t 3 others

ORIGIN

Query Match 96.7%; Score 228.2; DB 9; Length 698;
 Host Local Similarity 98.7%; Prod. No. 1.2e-47;
 Matches 230; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

UY 2 TTTGATTCATTCGCTTAATTAATTCAGGCGGTAACAGACAGTCTGTAAGAG 61
 |||
 db 233 TTTATTCATTCGCTTAATTAATTCAGGCGGTAACAGACAGTCTGTAAGAG 174
 62 CTTAGTTTAAAGCTATGATTAATTAATTCAGTCTGCTGCTGCTTAATCA 121
 |||
 db 173 CTTAGTTTAAAGCTATGATTAATTCAGTCTGCTGCTGCTTAATCA 114
 122 AGTCTTAAATTAAGCTGAATAATATACCTTAAATTAATTAATGCAATATTATA 181
 |||
 db 113 AGTCTTAAATTAAGCTGAATAATATACCTTAAATTAATTAATGCAATATTATA 54
 182 AATGACCAATATGATGCTGTAAGCTGCTGAATAATTAATTCAGTCGAGAGAA 234
 |||
 db 53 AATGACCAATATGATGCTGTAAGCTGCTGAATAATTAATTCAGTCGAGAGAA 1

RESULT 10
 AA924615/c 324 bp mRNA linear EST 29-APR-1998
 LOCUS 10998103.81 NCL-CCAP-Colo Homo sapiens cDNA clone IMAGE:1160333 3
 DEFINITION Similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN); mRNA
 sequence.

ACCESSION AA924615
 VERSION AA924615.1 GI:3070924
 KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Dan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 cDNA Library Preparation: M. Beutle Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CCAP clone distribution information can be

found through the J.M.A.G.B. Consortium/ILNC at: www.bio.uth.tmc.edu/bhrp/imagc/imagc.html
 Insert Length: 1123 Std Error: 0.00
 Seq primer: 40m3 fwd, 5' from Amersham
 High quality sequence stop: 214.
 Location/Qualifiers

FEATURES

SOURCE

1..424
 /organism "Homo sapiens"
 /db_xref "taxon:9606"
 /clone "IMAGE:1160333"
 /clone_lib "NCI-CCAP COL4"
 /issue_type "colon tumor REB"
 /lab_host "DH10B"
 /note "organ: colon; Vector: pT7-10-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from REB colon tumor, and was then primed with a Not I - oligo(dT) primer. Double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Beutle Soares and M. Fulina Bonaldo (N-Source4)."

BASE COUNT 117 a 55 c 57 g 95 t

ORIGIN

Query Match 96.5%; Score 227.8; DB 9; Length 424;
 Host Local Similarity 99.1%; Prod. No. 1.4e-47;
 Matches 229; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

UY 2 TTTGATTCATTCGCTTAATTAATTCAGGCGGTAACAGACAGTCTGTAAGAG 61
 |||
 db 233 TTTATTCATTCGCTTAATTAATTCAGGCGGTAACAGACAGTCTGTAAGAG 172
 62 CTTAGTTTAAAGCTATGATTAATTAATTCAGTCTGCTGCTGCTTAATCA 121
 |||
 db 171 CTTAGTTTAAAGCTATGATTAATTCAGTCTGCTGCTGCTTAATCA 112
 122 AGTCTTAAATTAAGCTGAATAATATACCTTAAATTAATTAATGCAATATTATA 181
 |||
 db 111 AGTCTTAAATTAAGCTGAATAATATACCTTAAATTAATTAATGCAATATTATA 52
 182 AATGACCAATATGATGCTGTAAGCTGCTGAATAATTAATTCAGTCGAGAG 234
 |||
 db 51 AATGACCAATATGATGCTGTAAGCTGCTGAATAATTAATTCAGTCGAGAG 1

RESULT 11
 A1678441/c 528 bp mRNA linear EST 15-DEC-1999
 LOCUS 1082401.x1 NCL-CCAP-Gas4 Homo sapiens cDNA clone IMAGE:2257537 3
 DEFINITION Similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN); mRNA
 sequence.

ACCESSION A1678441
 VERSION A1678441.1 GI:4888623
 KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CCAP clone distribution information can be found through the J.M.A.G.B. Consortium/ILNC at: www.bio.uth.tmc.edu/bhrp/imagc/imagc.html

Possible reversed clone: polyt not found
Seq primer: -400p from glibco
High quality sequence stop: 399.
Location/Qualifiers

FEATURES
source 1..618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2801425"
/clone_lib "NCI-CCAP_C014"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; Salt:
Site: 2; Nott: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"

BASE COUNT 193 a 121 c 137 g 167 t
ORIGIN

Query Match 95.8%; Score 226.2; DB 10; Length 618;
Best local Similarity 98.7%; Pred. No. 3.8e-47;
Matches 228; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY      2  TTTCATTCATGGCTTAATTAATCAAGGAGGCAAGAGTAGACAGTCTCTGTAAAGAG 61
        |||
DB      231 TTTCATTCATGGCTTAATTAATCAAGGAGGCAAGAGTAGACAGTCTCTGTAAAGAG 172

QY      62  CTTAGTTTAAATAGCTAAGCAATTCATTTGGACTGCTGTGCTCTCTTTAAATCA 121
        |||
DB      171 CTTAGTTTAAATAGCTAAGCAATTCATTTGGACTGCTGTGCTCTCTTTAAATCA 112

QY      122 AGTCCTTAATTAAGCTGAAAATATATAGCTCAGATTATTAAATGGAAATTATATA 181
        |||
DB      111 AGTCCTTAATTAAGCTGAAAATATATAGCTCAGATTATTAAATGGAAATTATATA 52

QY      182 AATGACCAATATGATACCTTTCAATGCTGTGCAATTAAGCTTCACTGGAAG 232
        |||
DB      51 AATGACCAATATGATACCTTTCAATGCTGTGCAATTAAGCTTCACTGGAAG 1

```

Search completed: March 17, 2003, 19:52:40
Job time : 1478 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

om nucleic - nucleic search, using sw model

Run on: March 17, 2003, 20:34:55 ; Search time 1462 Seconds
(without alignments)
2614.319 Million cell updates/sec

Title: US-09-247-874c-2_COPY_8710_8945

Perfect score: 236
Sequence: 1 tttagatcattgctcatt.....ataacttcactuaaaaaa 236

Scoring table: OLIGO_NDC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmva:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: qb_est1:*
10: qb_est2:*
11: qb_hic:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
15: em_estfun:*
16: em_estcom:*
17: qb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	189	80.1	324 9	AA923615 ng98b03.s
C 2	189	80.1	413 14	W38319 zc77b02.s1
C 3	189	80.1	514 9	AA131744 z135f02.s
C 4	189	80.1	521 9	AI022364 ow64g05.x
C 5	189	80.1	528 9	AI678441 iu82d01.x
C 6	189	80.1	548 14	BM997237 UF-H-DHO-BM997237

C 7	189	80.1	554 9	AA57318 um89a08.s
C 8	189	80.1	618 10	AA273081 x427h01.x
C 9	189	80.1	703 14	H0001221 U1-H-DH1-
C 10	189	80.1	770 14	H0000281 U1-H-DH1-
C 11	189	80.1	917 9	A1609005 tW85g07.x
C 12	189	80.1	911 12	BC194765 RST14064
C 13	147	62.3	549 9	A1566931 t67b02.x
C 14	147	62.3	746 13	B1519707 603061928
C 15	143	60.6	793 14	BM999417 U1-H-DH0-
C 16	138	58.5	314 9	AA382165 HS195428
C 17	138	58.5	375 12	BC119263 602349146
C 18	136	58.5	698 9	A1471571 t198b09.x
C 19	136	57.6	429 14	T29172 EST72706 HU
C 20	130	55.1	415 9	AA62146 EST1810
C 21	130	55.1	749 12	H6117168 H0117168 60234446
C 22	125	53.0	454 14	D20737 H00501714
C 23	124	52.5	223 9	AA362379 EST1846
C 24	113	47.9	619 10	AA953756 EST365826
C 25	108	45.8	430 14	MA7101 ZC39B04.s1
C 26	107	45.3	196 9	AA362067 EST1531
C 27	97	41.1	241 14	C06317 C06317 Huma
C 28	93	39.4	286 10	BE183186 RC4-H1066
C 29	61	25.8	925 10	BE19601 603472701
C 30	51	21.6	252 10	AA779422 h094a09.x
C 31	31	13.1	259 12	BS058513 h0115b02
C 32	28	11.9	265 10	BE184137 RC4-H1066
C 33	24	10.2	703 10	AV715451 AV715451
C 34	23	9.7	360 9	AA916006 c06b607.s
C 35	22	9.3	559 17	BS5984295 R097371R
C 36	20	8.5	685 17	AG163910 AG163910 Pan t10q1
C 37	20	8.5	993 14	CNS0606R C54301 C53301 Yuj1
C 38	19	8.1	300 14	C53301 C53301 Yuj1
C 39	19	8.1	381 17	AA236878 RPT1-21-9
C 40	19	8.1	463 13	H0148984 H0148984
C 41	19	8.1	476 14	BM864065 m06m06x8B
C 42	19	8.1	583 17	BM674814 BM674814
C 43	19	8.1	615 17	AA036473 HS-5052_B
C 44	19	8.1	646 12	BS803864 m06t001xm
C 45	19	8.1	661 10	AV702246 AV702246

ALIGNMENTS

RESULT 1
AA923615/c 324 bp mRNA linear EST 29 Apr 1998
ng98b03.s1 NCI-CCAP_Colo Homo sapiens cDNA clone IMAGE:1160333.3
similar to gb:U15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.

ACCESSION
AA923615
VERSION
AA923615.1 GI:3070924
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 324)
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE
NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap/
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Unpublished (1997)
CONTACT
Contact: Robert Strausberg, Ph.D.
Email: ccgaps-1@mail.nih.gov
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/INM at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1123 Std Error: 0.00

Seq primer: 40ml3 fwd, E1 from AmerSham
High quality sequence stop: 214.
Location/Qualifiers
1. 324

FEATURES
Source
/organism: "Homo sapiens"
/db_xref: "taxon:9606"
/clone_1lb: "MCL_GAP_Col0"
/issue_type: "colon tumor RER"
/lab_host: "DH10B"
Note: "organ: colon; Vector: pTZ19-Pac (pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER colon tumor, and was then primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptions (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library is normalized. Library was constructed by Benito Soares and M. Fatima Bonaldo (N Soares4)."
BASE COUNT 117 a 55 c 57 g 95 t
ORIGIN

Query Match 80.18; Score 189; 108 92 Length 324;
Best local similarity 100.0%; Prod. No. 76-94;
Matches 189; conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 ATTGATGGCTGATTTATTCGAAGGGGCGAAGAGTGCCTGCTTAAGAGAGCTTA 65
227 ATTATGGCTGATTTATTCGAAGGGGCGAAGAGTGCCTGCTTAAGAGAGCTTA 168
66 GTTTTATAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 125
167 GTTATTAAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 108
66 GTTTTATAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 125
126 GTTATTAAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 185
107 GTTATTAAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 48
186 AGCAAAATAT 194
47 AGCAAAATAT 49

RESULT 2
W88419/c 413 bp mRNA linear EST 15-MAY-1996
DEFINITION
287702.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328299 47
similar to gb:U15340 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.
W88419
ACCESSION
W88419.1 GI:119944
VERSION
W88419.1 GI:119944
KEYWORDS
EST
ORGANISM
human;
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 413)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapello, L.B.,
Thussis, S., Dierich, N., Dubugue, T., Favallo, A., Gish, W., Hawkins,
M., Holtzman, M., Kucuba, T., Lacy, M., Le, M., Le, N., Martins, E., Moore,
J.B., Morris, M., Parsons, J., Prange, C., Rikkin, L., Rohlfing, P.,
Schellander, K., Soares, M.B., Tan, F., Thier, M., Trevisan, E.,
Underwood, K., Weidmann, P., Waterston, R., Wilson, R. and Wurtz, M.
Generation and analysis of 280,000 human expressed sequence tags
from human testis (9), 807-828 (1996)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royally-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mb, RECAAT
High quality sequence stop: 368.
Location/Qualifiers
1. 413

FEATURES
Source
/organism: "Homo sapiens"
/db_xref: "taxon:9606"
/db_xref: "IMAGE:328299"
/clone_1lb: "pancreatic islet"
/issue_type: "pancreatic islet"
/lab_host: "Salk cells (kanamycin resistant)"
Note: "organ: pancreas; Vector: phage vector SK+ Site 1;
EcoRI Site 2; XhoI; Reference: Hum Mol Gen 2, 1795 (1993)
Takeda et al. Cloned and functionally primed; oligo dT
5' adaptor sequence 5' GAAATGGGAGG 3' 4' adaptor
sequence 5' GCAAGTCTTTTCTTTT 3' "
BASE COUNT 135 a 65 c 86 g 127 t
ORIGIN

Query Match 80.18; Score 189; 108 14; Length 413;
Best local similarity 100.0%; Prod. No. 7-20-94;
Matches 189; conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 ATTGATGGCTGATTTATTCGAAGGGGCGAAGAGTGCCTGCTTAAGAGAGCTTA 65
239 ATTATGGCTGATTTATTCGAAGGGGCGAAGAGTGCCTGCTTAAGAGAGCTTA 180
66 GTTTTATAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 125
179 GTTTTATAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 120
66 GTTTTATAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 125
126 GTTATTAAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 185
119 GTTATTAAGCTATGGAATCAATTCATTTGACCTGCTGCTCTTAAATCAAGTC 60
186 AGCAAAATAT 194
59 AGCAAAATAT 51

RESULT 3
AA131744/c 514 bp mRNA linear EST 27-NOV-1996
LOCUS
DEFINITION
2135102.s1 Soares_pregnant_adipose NIH3T3 Homo sapiens cDNA clone
IMAGE:503931 47 similar to gb:U15340 INTERLEUKIN-1 BETA PRECURSOR
(HUMAN);, mRNA sequence.
AA131744
ACCESSION
AA131744.1 GI:1693270
VERSION
AA131744.1 GI:1693270
KEYWORDS
EST
ORGANISM
human;
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 514)
Hillier, L., Clark, R., Dubugue, T., Ellstrand, K., Hawkins, M., Holtzman,
M., Holtzman, M., Kucuba, T., Le, M., Lennon, G., Matra, M., Parsons, J.,
Rikkin, L., Rohlfing, P., Soares, M.B., Tan, F., Trevisan, E., Waterston,
R., Williamson, A., Weidmann, P. and Wilson, R.
The WashU-Morck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royally-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 40ml3 fwd, from AmerSham
High quality sequence stop: 277.
Location/Qualifiers
1. 514
/organism: "Homo sapiens"

FEATURES
Source

```

/db_xref="CDB:3808919"
/db_xref="taxon:9606"
/clone_lib="IMAGE:503931"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex "female"
/dev_stage="adult"
/ab_host="DH10B"
/Note="Organ: uterus; Vector: p713-Pac; Site: 1; Not 1;
Site 2: Eco RI; 1st strand cDNA was primed with a Not 1 -
oligo(dT) primer [5',
AACTGAGAGAAATTCGGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not 1 and cloned into the Not 1
and Eco RI sites of the modified p713 vector. Library
went through one round of normalization. Library
constructed by M. Paloma Bonaldo."

BASE COUNT      156 a      85 c      114 g      149 t      10 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  ATTCATTGCTCAATTATTCAGAGCGCGCAGACAGTACAGTGTCTGTAAGAGACCTA 65
        |||||||
DB      244 ATTCATTGCTCAATTATTCAGAGCGCGCAGACAGTACAGTGTCTGTAAGAGACCTA 185

QY      66  GTTTTAAAGCTATGCAATTCATTGACGTGTGCTCTCTTTAAATCAAGTC 125
        |||||||
DB      184 GTTTTAAAGCTATGCAATTCATTGACGTGTGCTCTCTCTTTAAATCAAGTC 125

QY      126 GTTTTAAAGCTATGCAATTCATTGACGTGTGCTCTCTCTTTAAATCAAGTC 185
        |||||||
DB      124 GTTTTAAAGCTATGCAATTCATTGACGTGTGCTCTCTCTTTAAATCAAGTC 65

QY      186 AGCAAAATAT 194
        |||||||
DB      64 AGCAAAATAT 56

RESULT 4
LOCUS      A1022364          521 bp      mRNA      linear      EST 28-AUG-1998
DEFINITION 066405.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1651640 3' similar to gb:U5130 INTERLEUKIN-1 BETA
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION  A1022364
VERSION     A1022364.1  GI:3237605
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 521)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaaps@mail.nih.gov
            This clone is available royalty-free through LBNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1077 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amer sham
            High quality sequence stop: 403.
FEATURES
            1..521
            Location/Qualifiers
                1..521
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="IMAGE:1651640"
                /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                /issue_type="senescent fibroblast"
                /lab_host="DH10B (ampicillin resistant)"

```

```

/Note="Vector: p713) (Pharmacia) with a modified
polylinker V-type; phagemid; Site 1: Not 1; Site 2: Eco RI
polylinker cDNA was primed with a Not 1 - oligo(dT)
primer [5',
TGTACCAATCTGGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not 1 and cloned into
the Not 1 and Eco RI sites of a modified p713 vector
(Pharmacia). Library went through one round of
normalization to a Col - 5. Library constructed by Benito
Soares and M. Paloma Bonaldo."

BASE COUNT      165 a      92 c      123 g      141 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  ATTCATTGCTCAATTATTCAGAGCGCGCAGACAGTACAGTGTCTGTAAGAGACCTA 65
        |||||||
DB      232 ATTCATTGCTCAATTATTCAGAGCGCGCAGACAGTACAGTGTCTGTAAGAGACCTA 174

QY      66  GTTTTAAAGCTATGCAATTCATTGACGTGTGCTCTCTTTAAATCAAGTC 125
        |||||||
DB      172 GTTTTAAAGCTATGCAATTCATTGACGTGTGCTCTCTCTTTAAATCAAGTC 113

QY      126 GTTTTAAAGCTATGCAATTCATTGACGTGTGCTCTCTTTAAATCAAGTC 185
        |||||||
DB      112 GTTTTAAAGCTATGCAATTCATTGACGTGTGCTCTCTTTAAATCAAGTC 53

QY      186 AGCAAAATAT 194
        |||||||
DB      52 AGCAAAATAT 44

RESULT 5
LOCUS      A1678441          528 bp      mRNA      linear      EST 15-DEC-1994
DEFINITION 708201.x1 NCI-CGAP_Gas4 Homo sapiens cDNA clone IMAGE:225737 3'
            similar to gb:U5130 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
            sequence.
ACCESSION  A1678441
VERSION     A1678441.1  GI:4888623
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 528)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaaps@mail.nih.gov
            Tissue Procurement: Christopher Meskalko, M.D., Ph.D., Michael R
            Emmert-Buck, M.D., Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            found through the T.M.A.G.P. Consortium/LLNL at:
            www.bio.llnl.gov/btrp/image/image.html
            Insert Length: 1763 Std Error: 0.00
            Seq primer: -40up from gibco
            High quality sequence stop: 404.
FEATURES
            1..528
            Location/Qualifiers
                1..528
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="IMAGE:225737"
                /clone_lib="NCI-CGAP_Gas4"
                /issue_type="poorly differentiated adenocarcinoma with

```



```

/tissue_type="colon tumor RER-"
/lab_host="DRI08"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(dI) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo (Soares4
).
"
BASE COUNT      176 a      97 c      126 g      154 t      1 others
ORIGIN
Query Match      80.1%; Score 189; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 7.5e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATGCGCTGATTTATTCAGAGGGGGCAGAGTGCAGTGTGTAAGAGAGCCCA 65
DB 241 ATTCATGCGCTGATTTATTCAGAGGGGGCAGAGTGCAGTGTGTAAGAGAGCCCA 172
QY 65 GTTTTAATAGCTATGATCAATTCATTCATTCGAGTGTGCTCTCTTAATCAAGTC 125
DB 171 GTTTTAATAGCTATGATCAATTCATTCATTCGAGTGTGCTCTCTTAATCAAGTC 112
QY 126 GTTTTAATAGCTATGATCAATTCATTCATTCGAGTGTGCTCTCTTAATCAAGTC 185
DB 111 GTTTTAATAGCTATGATCAATTCATTCATTCGAGTGTGCTCTCTTAATCAAGTC 52
QY 186 ACCAAATAT 194
DB 51 ACCAAATAT 43

RESULT 8
AM273081/c
LOCUS      AM273081 618 bp mRNA linear EST_03-JAN-2000
DEFINITION x027h01.x1 NCI-CCAP_Co14 Homo sapiens cDNA clone IMAGE:2801425 3'
similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN); mRNA
sequence.
ACCESSION  AM273081
VERSION     AM273081.1 GI:6660111
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR INDEX Unpublished (1997)
AUTHORS     Contact: Robert Strausberg, Ph.D.
              Email: rgaaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Barnett-Fuck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMIL at:
www.bio.lnrl.gov/bdrip/image/image.html

FEATURES
Source
1..618
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2801425"
/clone_lib="NCI-CCAP_Co14"

```

```

/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DRI08"
/note="Organ: colon; Vector: pCMV-SpR6th; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally; Primer: oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
BASE COUNT      193 a      121 c      137 g      167 t
ORIGIN
Query Match      80.1%; Score 189; DB 10; Length 618.
Best Local Similarity 100.0%; Pred. No. 7.6e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATGCGCTGATTTATTCAGAGGGGGCAGAGTGCAGTGTGTAAGAGAGCCCA 65
DB 227 ATTCATGCGCTGATTTATTCAGAGGGGGCAGAGTGCAGTGTGTAAGAGAGCCCA 168
QY 66 GTTTTAATAGCTATGATCAATTCATTCATTCGAGTGTGCTCTCTTAATCAAGTC 125
DB 167 GTTTTAATAGCTATGATCAATTCATTCATTCGAGTGTGCTCTCTTAATCAAGTC 108
QY 126 GTTTTAATAGCTATGATCAATTCATTCATTCGAGTGTGCTCTCTTAATCAAGTC 185
DB 107 GTTTTAATAGCTATGATCAATTCATTCATTCGAGTGTGCTCTCTTAATCAAGTC 48
QY 186 ACCAAATAT 194
DB 47 ACCAAATAT 39

RESULT 9
HQ001221/c
LOCUS      HQ001221 703 bp mRNA linear EST_17 JUN 2002
DEFINITION U1-H-DH1-awp-g-21-0-01.s1 NCI-CCAP-DH1 Homo sapiens cDNA clone
IMAGE:5892524 3', mRNA sequence.
ACCESSION  HQ001221
VERSION     HQ001221.1 GI:19726121
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR INDEX Unpublished (1997)
AUTHORS     Contact: Robert Strausberg, Ph.D.
              Email: rgaaps-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/ILMIL at: http://image.lnrl.gov
sequence: 221-272, >(TAA)A)n*Simple.Repeat
Seq primer: M13 FORWARD
POLY-A=yes.

FEATURES
Source
1..703
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5892524"
/clone_lib="NCI-CCAP-DH1"
/tissue_type="Metastatic Chondrosarcoma"
/seq_strategy="Aduit"
/lab_host="DRI08 (Life Technologies)"
/note="Organ: Lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI-CCAP-DH1 is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed

```


differentiated (4 pooled tumors, including primary and metastatic)

cloning). Average insert size 1.7 kb, insert size range 1.2-4.3 kb. Library is normalized and enriched for full-length clones and was constructed by G. Gruber (University of Toronto). Research clones tracking code 027. Note: this is a NIH_MGC library.

/dev_stage="adult"

1.2-4.3 kb. Library is normalized and enriched for full-length clones and was constructed by G. Gruber (University of Toronto). Research clones tracking code 027. Note: this is a NIH_MGC library.

/note_borgan: lung; Vector: pTZ19-pac (pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Palma-Bouabou.

cloning). Average insert size 1.7 kb, insert size range 1.2-4.3 kb. Library is normalized and enriched for full-length clones and was constructed by G. Gruber (University of Toronto). Research clones tracking code 027. Note: this is a NIH_MGC library.

BASE COUNT 173 a 107 c 119 g 149 t 1 others

BASE COUNT 206 a 158 c 177 g 205 t

Query Match 62.3%; Score 147; DB 9; Length 549;

Query Match 62.3%; Score 147; DB 13; Length 746;

Host Local Similarity 100.0%; Pred. No. 9, 10-70;

Host Local Similarity 100.0%; Pred. No. 9, 10-70;

Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 48 TGTGTGTAAGAAAGAGGATTTTAAAGCTTAAGCAATCAATTCAGTCTGCTG 107

DB 126 GTTAAATTACAGCGAATAATATAA 152

DB 186 TGTGTGTAAGAAAGAGGATTTTAAAGCTTAAGCAATCAATTCAGTCTGCTG 127

DB 28 CTTAAATTACAGCGAATAATATAA 2

DB 108 CTTCTTTAAATCAAGTCTTTAATTAAGCTGAATAATTAAGCTGACATT 167

DB 148 ATGATGTCCTAATTTATTAAGAGAGAGAAAGATAGAGTCTGTAAGAAATCA 65

DB 126 CTTCTTTAAATCAAGTCTTTAATTAAGCTGAATAATTAAGCTGACATT 67

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 168 TGGCAATATTTAAAGAGCAATAT 194

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

DB 66 TGGCAATATTTAAAGAGCAATAT 40

DB 88 GTTTTAAATACGTAATGAAATCAATTAATTAAGCTGACATTGCTGCTGCTGCTG 29

a library tag sequence that is located between the Not I
site and the (GT)₁₈ tail. The sequence tag for this
library is GTCTACGAG.

TAG_LIB=UT-H-DPO

TAG_TISSUE=fibrosarcoma

TAG_SEQ=GTCTACGAG*

BASE COUNT 224 a 154 c 181 g 231 t 3 others

ORIGIN

Query Match

60.6%; Score 143; DB 14; length 793;

Best Local Similarity 100.0%; Pred. No. 1.5e-67;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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UY 6 ATTGATTGGTCTAATTTATTCACAGCGGCGAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 240 ATTGATTGGTCTAATTTATTCACAGCGGCGAGAGTAGCAGTGTCTGTAAAGAGCCTA 181
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
UY 66 GTTTTAATAGCTATGCAATTCATTTGACTGCTGCTGCTGCTTAATCAAGTC 125
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180 GTTTTAATAGCTATGCAATTCATTTGACTGCTGCTGCTGCTGCTTAATCAAGTC 121
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
UY 126 CTTTAATTAGACTGAAATATA 148
    ||||||||||||||||||||||||
Db 120 CTTTAATTAGACTGAAATATA 98
    ||||||||||||||||||||||||

```

Search completed: March 17, 2003, 21:29:38
Job time : 1444 secs

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•

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nuclei - nucleic search, using sw model

Run on: March 17, 2003, 19:52:45 ; Search time 224 seconds

Title: US-09-247-874C-2_COPY_8710_8945

Sequence: 1 ttltgattcaattgtctaat.....ataacttcaactgaagaaa 236

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

word size :

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000000

Post-processing: listing first 45 summaries

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23: /SIDS2/qcadata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/qcadata/geneseq/geneseqn-emb1/NA2002.DAT.*
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SUMMARY

Result No.	Score	Query Match	Length	EB	ID	Description
1	236	100.0	9721	21	AAA50175	Human interleukin
2	194	82.2	656	21	AAA51859	Interleukin 1-beta
3	194	82.2	1456	21	AAI20946	Human interleukin
4	194	82.2	1456	21	AAA34824	Human adenosine r
5	194	82.2	1507	6	AAO50600	Sequence encoding
6	194	82.2	1507	14	AAO50981	Human interleukin
7	194	82.2	9721	20	AAI25924	Human interleukin
8	194	82.2	9721	21	AAI20945	Human interleukin
9	194	82.2	9721	21	AAO61768	Human IL-1b gene.

[illegible]

|||||
 Db 549 AAGTCTTTAAATTAACACGAAATATATAACGTCAGATATTAAATGCAATATTAT 608
 QY 181 AATATGCAATATAT 194
 Db 609 AATATGCAATATAT 622
 RESULT 3
 AAF20946
 ID AAF20946 standard; DNA: 1496 BP.
 XX
 AC AAF20946;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human interleukin-1 polynucleotide fragment #2513.
 XX
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antisthmatic; analgesic; hypotensive; cyclostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; SS.
 XX
 OS Homo sapiens.
 XX
 PN WD2000b2736-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-DS08020.
 XX
 XX 06-APR-1999; 9905-012795d.
 XX
 XX (UWEC-) UNIV EAST CAROLINA.
 XX (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 XX
 XX WPI: 2000-679539/66.
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Disclosure: Page 232-233; 1592pp; English.
 XX
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (1) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antisthmatic, hypotensive and cyclostatic activities.
 CC The antisense oligonucleotides and (1) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18414 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 XX Sequence 1496 BP: 416 A; 361 C; 328 G; 391 T; 0 other:
 SO
 Query Match 82.2%; Score 194; DF 21; Length 1496;
 Best Local Similarity 100.0%; Pred. No. 13e-85;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTGATTCATTCGCTGCTAATTTATTCGAAAGGGGCGAAGACTAGCATGTGTGTAANCA 60
 Db 1269 TTTTGATTCATTCGCTGCTAATTTATTCGAAAGGGGCGAAGACTAGCATGTGTGTAANCA 1328
 QY 61 GCGTAGTTTAAATAGCTATGCAATTCGATTTGAGCTGCTGCTCTTAATTC 120
 Db 1329 GCGTAGTTTAAATAGCTATGCAATTCGATTTGAGCTGCTGCTCTTAATTC 1388
 QY 121 AAGTCCTTTAATTAAGACTGAAATATATTAAGCTGCAATTTAAATGGCAATATTTAA 180
 Db 1389 AAGTCCTTTAATTAAGACTGAAATATATTAAGCTGCAATTTAAATGGCAATATTTAA 1448
 QY 181 AATATGCAATATAT 194
 Db 1449 AATATGCAATATAT 1462
 RESULT 4
 ID AAF34824 standard; DNA: 1496 BP.
 XX
 XX AAF34824;
 XX
 XX 28-JUL-2000 (first entry)
 XX
 XX Human adenosine receptor related polynucleotide SEQ ID No:2513.
 XX
 XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antisthmatic; cyclostatic; analgesic; impeded airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; SS.
 XX
 XX Homo sapiens.
 OS
 PN WD200009525-A2.
 XX
 XX 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US17712.
 XX
 XX 03-AUG-1998; 98US-0095212.
 XX
 XX (UWEC-) UNIV EAST CAROLINA.
 XX
 XX Nyce JW;
 XX
 XX WPI: 2000-205971/18.
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischaemia or
 PT cancers -
 XX
 XX Disclosure: Page 675; 1343pp; English.

XX The present invention describes a new composition comprising an
 CC antihemophilic acid (AH) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The AH can have anti-inflammatory, antiallergic,
 CC and/or immunomodulatory, cytosolic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects affect the lungs of a subject. They can be used for treating
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the AH reduces side effects. The A-containing AHs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AA32413 to AA45412 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 185, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AA45413 to AA45992) are specifically claimed AHs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other;

XX Query Match 82.2%; Score 194; DB 21; Length 1496;
 XX Best Local Similarity 100.0%; Pred. No. 1 to 85;

XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TTTTGGTATGCTGGCTATTTATTCAGAGGGGCGAGAGTACGATCTCTTAAGA 60
 DB 1269 TTTTATCATTTGCTATTTATTTCAAGGGGCGAGAGTACGATCTCTTAAGA 1328
 YY 61 GCTTACTTTTATGATGATGATTAATTCATTTGATGCTGCTCTTTAATTC 120
 DB 1329 GCTTACTTTTATGATGATGATTAATTCATTTGATGCTGCTCTTTAATTC 1388
 YY 121 AAGCTCTTAAATTAAGATGAAATATATATATATATATATATATATATATAT 180
 DB 1389 AAGCTCTTAAATTAAGATGAAATATATATATATATATATATATATATAT 1448
 YY 181 AATATGCGAATAT 194
 DB 1449 AATATGCGAATAT 1462

XX RESULT 5
 XX ID AAN50060 standard; cDNA; 1507 BP;
 XX AN AAN50060;

XX 09 SEP-1991 (first entry)

XX Sequence encoding interleukin-1 (IL-1).

XX Immunological reagent: T cell stimulant; B cell; immunoglobulin; ss.

XX Homo sapiens.

XX Key location/Qualifiers

XX Key 87-894

XX Key 87-894

XX Key 87-894

XX Key 87-894

XX 11-FEB-1985; 8505-0700374.
 XX (NME) NEW ENGLAND MED GEN.
 XX AUCON PE, Webb AC, Goltke L, DiMartino CA, Rossmasser L, Rich A;
 XX Wollt SM;
 XX WPI: 1985-291135/47.
 XX P-PSDH: AAN50043.
 XX Recombinant cloning vehicle contg human interleukin 7 gene or its
 XX fragments, producing new biologically active polypeptide(s)
 XX claim 7: page 34-35; 39pp; Eng118b.
 XX A pure cDNA of 1507 bp (AAN50060) (and its 1-606, 1-677, 1-655, 1507;
 XX 482, 1501; 482, 677; and 1-655-1507 fragments) are claimed. Also
 XX claimed is a recombinant DNA cloning vehicle contg. The human IL-1
 XX gene sequence. Specifically the vehicle contains the sequence coding
 XX for the new 287 AA sequence (AAN50043) or the following new fragments
 XX (1) 9-224; (2) 1-210-X; (3) 144-287; and (4) 144-210-X; (X=Asn
 XX Ser-Tyr-Thr-Gly-Val-Ileu Ser-Ileu Asn-Gln-Val-Ileu).
 XX Sequence 1507 BP; 427 A; 461 C; 328 G; 391 T; 0 other;

XX Query Match 82.2%; Score 194; DB 6; Length 1507;
 XX Best Local Similarity 100.0%; Pred. No. 1 to 85;

XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TTTTGGTATGCTGGCTATTTATTCAGAGGGGCGAGAGTACGATCTCTTAAGA 60
 DB 1269 TTTTATCATTTGCTATTTATTTCAAGGGGCGAGAGTACGATCTCTTAAGA 1328
 YY 61 GCTTACTTTTATGATGATGATTAATTCATTTGATGCTGCTCTTTAATTC 120
 DB 1329 GCTTACTTTTATGATGATGATTAATTCATTTGATGCTGCTCTTTAATTC 1388
 YY 121 AAGCTCTTAAATTAAGATGAAATATATATATATATATATATATATATATAT 180
 DB 1389 AAGCTCTTAAATTAAGATGAAATATATATATATATATATATATATATAT 1448
 YY 181 AATATGCGAATAT 194
 DB 1449 AATATGCGAATAT 1462

XX RESULT 6
 XX ID AAN50981 standard; cDNA; 1507 BP;
 XX AN AAN50981;

XX 19-MAY-1994 (first entry)

XX human interleukin 1 coding sequence.

XX hIL-1; interleukin; cytokine; truncated; N-terminal deletion;

XX C-terminal deletion; ss.

XX Homo sapiens.

XX Key location/Qualifiers

XX Key 87-896

XX Key 87-896

XX Key 87-896

XX Key 87-896

XX This sequence which contain IL-1 activity
 XX are covered by the invention.


```

XX 07-MAY-1985: 85EP-0303234.
XX 18-MAY-1984: 84US-0611669.
XX 11-FEB-1985: 85US-0700574.
XX (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX (NEW-) NEW ENGLAND MED. CENT HOSPITALS.
XX (TUFT) TUFTS COLLEGE.
XX (WELL-) WELLESLEY COLLEGE.
XX Atron PE, Dinarello CA, Gehlke L, Rich A, Rosenwasser LJ;
XX Webb AC, Wolff SM;
XX WPI: 1993-460975/46.
XX P-PSDB: AAR42213.
XX New DNA encoding protein with IL-1 activity - useful in
XX monitoring disease states e.g. cancer and studying inflammation
XX e.g. in arthritis etc.
XX Claim 1: Page 11-16: 24pp: English.
XX DNA comprising part of the nucleotide sequence AA050981 which encodes
XX a polypeptide having IL-1 activity and a mol wt. of 20000 is claimed.
XX Specifically, the region between nucleotides 111-717 has been found
XX to retain IL-1 activity (see AA045464).
XX Sequence 1507 BP: 427 A; 361 C; 328 G; 394 T; 0 other;
XX Query Match 82.2%; Score 194; DB 14; Length 1507;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-85;
XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 TTTGATTGATGGTGTAAATTATTCAGAGGAGGAGAGTGTGTGTAAAGA 60
XX 1269 TTTGATTGATGGTGTAAATTATTCAGAGGAGGAGAGTGTGTGTAAAGA 1328
XX 61 GCCTAGTTTAAATAGTATGATGATCAATTCATTGGAGCTGTGTCTTTAAATC 120
XX 1329 GCCTAGTTTAAATAGTATGATGATCAATTCATTGGAGCTGTGTCTTTAAATC 1388
XX 121 AAGCTCTTAAATAGTATGATGATCAATTCATTGGAGCTGTGTCTTTAAATC 180
XX 1389 AAGCTCTTAAATAGTATGATGATCAATTCATTGGAGCTGTGTCTTTAAATC 1448
XX 181 AATGAGCAAAATAT 194
XX 1449 AATGAGCAAAATAT 1462
XX
XX RESULT 7
XX AA075924
XX ID AAX75924 standard; DNA: 9721 BP.
XX AC AAX75924:
XX
XX 29-JUL-1999 (first entry)
XX Human interleukin 1A gene.
XX
XX Human interleukin 1: IL-1A; IL-1A; IL-1A; diagnosis; detection;
XX chronic obstructive airway disease; chronic bronchitis; emphysema;
XX asthma; chronic bronchitis; proinflammatory haplotype; ss.
XX Homo sapiens.
XX
XX W09924615-A2
XX
XX 20-MAY-1999.
XX
XX 09-NOV-1998: 98WO-0523721.
XX

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```

PR 12-JAN-1998: 98US-0005923.
PR 07-NOV-1997: 97GB-0023553.
XX
XX (MEDI-) MEDICAL SCI SYSTEMS INC.
XX Barnes PJ, Duff GW, Giovino M, Lim S;
XX WPI: 1999-327420/27.
XX
XX Genotyping nucleic acid samples for interleukin-1 (IL-1)
XX proinflammatory haplotype alleles, useful for predicting
XX susceptibility to developing chronic obstructive airway disease
XX
XX Example 1: Fig 2: 37pp: English.
XX
XX The present invention describes genotyping a nucleic acid sample from a
XX subject to determine at least one allele of an interleukin-1 (IL-1)
XX proinflammatory haplotype. A method has also been described for
XX determining a subject's susceptibility to developing chronic obstructive
XX airway disease (COAD) or for predicting the rapidly or ultimate
XX progression of a COAD in the subject by: (a) obtaining a nucleic acid
XX sample from the subject; and (b) detecting at least one allele of an
XX IL-1 proinflammatory haplotype in the sample, where detection of at
XX least one of these alleles indicates that the patient has an increased
XX susceptibility to developing COAD. The method is useful for determining
XX the susceptibility of subjects to developing chronic obstructive airway
XX disease or for predicting the rapidly or ultimate progression of
XX chronic obstructive airway disease (COAD). COAD can be asthma, emphysema,
XX chronic bronchitis or chronic obstructive airway disease (COAD).
XX early identification of chronic obstructive airway disease (COAD),
XX facilitating administration of appropriate treatment at the earliest
XX stage, thereby increasing the probability of a positive outcome. The
XX present sequence represents the human IL-1B gene.
XX
XX Sequence 9721 BP: 2662 A; 2328 C; 2121 G; 2608 T; 2 other;
XX Query Match 82.2%; Score 194; DB 20; Length 9721;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-85;
XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 TTTGATTGATGGTGTAAATTATTCAGAGGAGGAGAGTGTGTGTAAAGA 60
XX 8710 TTTGATTGATGGTGTAAATTATTCAGAGGAGGAGAGTGTGTGTAAAGA 8769
XX 61 GCCTAGTTTAAATAGTATGATGATCAATTCATTGGAGCTGTGTCTTTAAATC 120
XX 8770 GCCTAGTTTAAATAGTATGATGATCAATTCATTGGAGCTGTGTCTTTAAATC 8829
XX 121 AAGCTCTTAAATAGTATGATGATCAATTCATTGGAGCTGTGTCTTTAAATC 180
XX 8830 AAGCTCTTAAATAGTATGATGATCAATTCATTGGAGCTGTGTCTTTAAATC 8889
XX 181 AATGAGCAAAATAT 194
XX 8890 AATGAGCAAAATAT 8903
XX
XX RESULT 8
XX AAF20945
XX ID AAF20945 standard; DNA: 9721 BP.
XX AC AAF20945:
XX
XX 14-MAR-2001 (first entry)
XX Human interleukin-1 polynucleotide fragment #2512.
XX
XX low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX

```


QY 121 AAGTCCTTATTAGAGCTGAAAATATATAGCTCATGATTATTAAATGGAAATTATTAT 180
 |||
 DB 8830 AAGTCCTTATTAGAGCTGAAAATATATAGCTCATGATTATTAAATGGAAATTATTAT 8889
 QY 181 AATGAGCAAAATAT 194
 |||
 DB 8890 AATGAGCAAAATAT 8903
 RESULT 10
 ID AAA50174 standard; DNA: 9721 BP.
 XX AAA50174:
 AC
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human Interleukin-1 beta allele 1 (+6912).
 XX
 KW Interleukin-1 beta; IL-1b; human; polymorphism; inflammation;
 KW coronary artery disease; osteoporosis; nephropathy;
 KW alopecia areata; Graves disease; systemic lupus erythematosus;
 KW lichen sclerosus; ulcerative colitis; diabetic retinopathy;
 KW periodontal disease; juvenile chronic arthritis; psoriasis;
 KW insulin dependent diabetes; asthma; lung fibrosis;
 KW chronic inflammatory liver disease; rheumatoid arthritis;
 KW chronic inflammatory lung disease; antiinflammatory;
 KW dermatological; immunosuppressive; antidiabetic; antihypertoid;
 KW arthritic; antirheumatic; antiasthmatic; antipsoriatic;
 KW hepatotropic; antileuk; diagnosis; therapy; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT replacement(8904,G)
 FT variation
 FT /tag= a
 FT /note= "IL-1b allele 1 (+6912)"
 PN W0200047619-A1.
 XX
 PD 17-AUG-2000.
 XX
 PF 10-FEB-2000; 2000MO-0503443.
 XX
 PR 10-FEB-1999; 9905-0247874.
 XX
 PA (INT-) INTERLEUKIN GENETICS INC.
 XX
 PI Duff GW, Di Giovanni FS;
 XX
 DR WPI; 2000-558192/51.
 XX
 XX Novel methods and nucleic acids for diagnosing and treating disorders
 PI associated with high levels of interleukin beta, especially
 PT inflammatory diseases -
 PS
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC The present sequence is that of human interleukin-1 beta (IL-1b)
 CC allele 1 (+6912), which is a form of the IL-1b gene that contains
 CC cytosine at position +6912; IL-1b allele 2 (+6912) has guanine at
 CC this position (see AAA50175). The invention is based on the
 CC identification of this novel allele at marker +6912 of the IL-1b
 CC gene. The C to G transition occurs within the 3' untranslated
 CC region of the IL-1b gene and results in an increased level of IL-1b
 CC protein. Individuals homozygous for the IL-1b allele 2 (+6912)
 CC accumulate approximately 4 times more immunoreactive IL-1b protein
 CC than homozygotes for IL-1b allele 1 (+6912). Methods and kits are
 CC provided for detecting IL-1b allele 2 (+6912), or an allele in
 CC linkage disequilibrium with an IL-1b allele 2 (+6912), and
 CC thereby determining a patient's susceptibility to developing
 CC inflammatory disorders, especially coronary artery disease.

CC osteoporosis, nephropathy in diabetes mellitus, alopecia areata,
 CC Graves disease, systemic lupus erythematosus, lichen sclerosus,
 CC ulcerative colitis, diabetic retinopathy, periodontal disease,
 CC juvenile chronic arthritis, psoriasis, insulin dependent diabetes,
 CC asthma, chronic inflammatory liver disease, chronic inflammatory
 CC lung disease, lung fibrosis, and rheumatoid arthritis (claimed).
 CC Identification of the IL-1b allele 2 (+6912) and its involvement in
 CC IL-1b overproduction also enables screening assays for identifying
 CC IL-1b antagonists that can be used to treat conditions associated
 CC with IL-1b allele 2 (+6912). Transgenic animals are also claimed,
 CC and can be used to identify IL-1b agonists and antagonists, or
 CC to confirm the safety and efficacy of candidate therapeutics.
 XX
 SO Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other:
 Query Match 82.2%; Score 194; DB 21; Length 9721;
 Best local Similarity 100.0%; Pred. No. 1,36-85;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTGATTCATGCTCAATTTATTCAGAGGCGGCAAGATAGTCATGTCGTAAGAA 60
 |||
 DB 8710 TTTTGATTCATGCTCAATTTATTCAGAGGCGGCAAGATAGTCATGTCGTAAGAA 8769
 QY 61 GCGTAGTTTATAGCTATGAGATCAATTCATTTGGACTGGTGGCTGTTTAAATC 120
 |||
 DB 8770 GCGTAGTTTATAGCTATGAGATCAATTCATTTGGACTGGTGGCTGTTTAAATC 8829
 QY 121 AAGTCCTTATTAGAGCTGAAAATATATAGCTCATGATTATTAAATGGAAATTATTAT 180
 |||
 DB 8830 AAGTCCTTATTAGAGCTGAAAATATATAGCTCATGATTATTAAATGGAAATTATTAT 8889
 QY 181 AATGAGCAAAATAT 194
 |||
 DB 8890 AATGAGCAAAATAT 8903
 RESULT 11
 ID AAA34823 standard; DNA: 9721 BP.
 XX AAA34823:
 AC
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2512.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytoskeletal; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99MO-US17712.
 XX
 PR 03-AUG-1998; 9805-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 XX Now antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension.

Gencore version 5.1.4.p5_4578
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ol nucleic - nucleic search, using sw model

Run on: March 17, 2003, 20:32:40 ; Search time 1145 Seconds

(without alignments)
5998.482 Million cell updates/sec

Title: US-09-247-874c-2_COPY_8710_8945

Perfect score: 236
Sequence: 1 ttltgattcattgtctaat.....ataaacctcactgaagaata 236

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4104280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: listing first 45 summaries

Database :

1: gb_ba:*
2: gb_hg:*
3: gb_in:*
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6: gb_pat:*
7: gb_ph:*
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9: gb_pt:*
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40: gb_vl:*
41: gb_vl:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	82.2	614	11	G10509
2	194	82.2	656	6	AX027920
3	194	82.2	1459	6	101156
4	194	82.2	1496	9	HMM11
5	194	82.2	1496	9	HMM11
6	194	82.2	1507	6	E00846
7	194	82.2	1507	6	107942
8	194	82.2	5721	6	AX052806
9	194	82.2	9721	6	AX067266
10	194	82.2	9721	6	AX069435
11	194	82.2	9721	9	HSL1B
12	189	80.1	1382	6	AX19978
13	189	80.1	1473	9	HSPK11B
14	189	80.1	1497	6	AR030386
15	189	80.1	1497	6	E06714
16	189	80.1	1497	9	HMM11B
17	189	80.1	1522	9	BC008678
18	189	80.1	7824	9	HMM11B
19	189	80.1	17447	9	AT137079
20	189	80.1	154214	9	AC079753
21	132	55.9	1514	6	AR086959
22	132	55.9	1514	6	100729
23	121	51.3	1404	6	A21148
24	121	51.3	1404	6	E01230
25	121	51.3	1404	6	E11934
26	121	51.3	1404	6	E12090
27	121	51.3	1404	6	E12090
28	121	51.3	1404	6	E12090
29	121	51.3	1404	6	E12090
30	121	51.3	1404	6	E12090
31	121	51.3	1404	6	E12090
32	121	51.3	1404	6	E12090
33	121	51.3	1404	6	E12090
34	121	51.3	1404	6	E12090
35	121	51.3	1404	6	E12090
36	121	51.3	1404	6	E12090
37	121	51.3	1404	6	E12090
38	121	51.3	1404	6	E12090
39	121	51.3	1404	6	E12090
40	121	51.3	1404	6	E12090
41	121	51.3	1404	6	E12090
42	121	51.3	1404	6	E12090
43	121	51.3	1404	6	E12090
44	121	51.3	1404	6	E12090
45	121	51.3	1404	6	E12090

ALIGNMENTS

RESULT 1
G10509
LOCUS
DEFINITION
human STS CHLC.UTR_006699_X04500.p37183 clone UTR_006699_X04500,
sequence tagged site.
ACCESSION
G10509.1 GI:942358
VERSION
STS: STS sequence; primer: sequence tagged site.
KEYWORDS
Homo sapiens vector-pucl host-E.coli dna-ung- (initial) Mark1
SOURCE
Selected genomic DNA prepared from AT individual of French
nationality.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 614)

pred. No. is the number of results predicted by chance to have a

AUTHORS Murray, J., Sheffield, V., Weber, J.L., Day, G., and Butler, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1993)
SYNOPSIS DFR_00659_X04500, CMLC_DFR_00659_X04500.1 36097
CONTACT Dr. Jeffrey C. Murray

NOTE The University of Iowa
 Department of Pediatrics, Iowa City, IA 52242, USA
 Tel: (319) 356-3508
 Fax: (319) 356-3447
 Email: jcmurray@uiowa.edu

PRIMER A: AGTCACATCTCTCTTAAAGG
PRIMER B: CTCTGCTCTTCAATTAAT
STS SIZE: 229

PCR Protocol:
 denature: 30 seconds at 94 degrees C
 annealing: 75 seconds at 55 degrees C
 extension: 15 seconds at 72 degrees C
 PCR cycles: 27
 extension: 6 minutes at 72 degrees C

Template: 30ng genomic DNA
Primer: each 1.5 pmole
DNase: each 200 uM
Tag polymerase: 0.3 units
Total Vol: 10 uL

Buffer:
 MgCl₂: 1.5mM
 KCl: 50mM
 Tris: 10mM
 pH: 8.3

FEATURES Prepared with primer pairs derived from X04500.
 Location/Qualifiers

Source: 1..614
 Organism: "Homo sapiens"
 /db_xref="taxon:9606"
 SES
 Primer_Pair
 complement(189..408)
 base_count 174 a 156 c 120 g 184 t
 origin

Query Match 82.2% Score 194; DB 11; Length 614;
 Best Local Similarity 100.0%; Pred. No. 1,90-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 TTTGATTAATGGCTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTTAAGAA 60
 |||||||
 DB 371 TTTGATTAATGGCTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTTAAGAA 430
 UY 61 GCTTAACTTTTAAAGCTATGTAATCAATTCATTCATTCATTCATTCATTCATTC 120
 |||||||
 DB 441 GCTTAACTTTTAAAGCTATGTAATCAATTCATTCATTCATTCATTCATTCATTC 490
 UY 121 AATCTTTAATTAAGCAATTAATTAATTCAGATTAATTAATTAATTAATTAATTAAT 180
 |||||||
 DB 491 AATCTTTAATTAAGCAATTAATTAATTCAGATTAATTAATTAATTAATTAATTAAT 550

UY 181 AATTAACAAATAT 194
 |||||||
 DB 551 AATTAACAAATAT 564

RESULT 2
 AX027920 656 bp DNA linear PAT 16-SEP-2000
 DEFINITION Sequence 5 from Patient W00039314.
 AX027920
 AX027920.1 GI:10188746
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catartida; Hominoidea; Homo;

REFERENCE 1 (bases 1 to 656)

AUTHORS Kasperkiewicz, and Cheneval, J.

TITLE Assay for identifying compounds which affect stability of mRNA

JOURNAL Patient: W00039314-A 5, 06 JUN 2000

KASPERKIEWICZ, J. (CA) ; CHENEVAL, DOMINIQUE (CA) ; NOVATION
 PHARMACEUTICALS INC (CA)

FEATURES
 source
 1..656
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 176 a 151 c 129 g 200 t

Query Match 82.2% Score 194; DB 6; Length 656;
 Best Local Similarity 100.0%; Pred. No. 1,90-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 TTTGATTAATGGCTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTTAAGAA 60
 |||||||
 DB 429 TTTGATTAATGGCTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTTAAGAA 488
 UY 61 GCTTAACTTTTAAAGCTATGTAATCAATTCATTCATTCATTCATTCATTCATTC 120
 |||||||
 DB 489 GCTTAACTTTTAAAGCTATGTAATCAATTCATTCATTCATTCATTCATTCATTC 548
 UY 121 AATCTTTAATTAAGCAATTAATTAATTCAGATTAATTAATTAATTAATTAATTAAT 180
 |||||||
 DB 549 AATCTTTAATTAAGCAATTAATTAATTCAGATTAATTAATTAATTAATTAATTAAT 608

UY 181 AATTAACAAATAT 194
 |||||||
 DB 609 AATTAACAAATAT 622

RESULT 3
 LOCUS 101156 1469 bp ss-DNA linear PAT 21 MAY 1993
 DEFINITION Sequence 1 from Patient US 4762914.
 ACCESSION 101156
 VERSION 101156.1 GI:313921
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1469)
AUTHORS Auton, P.E., Webb, A.C., Geburke, L., Bhargava, A., Rosenwasser, L.J.,
 Ricca, A., and Wolff, S.M.

TITLE Truncated protein of interleukin-1

JOURNAL Patent: US 4762914-A 1 09 AUG 1988;

119 Wilson Dr.; Framingham, MA

on Jul 30, 1993. This sequence version replaced gi:285480.

COMMENT Location/Qualifiers
 source
 1..1469
 /organism="Unknown"

BASE COUNT 408 a 354 c 426 g 481 t

Query Match 82.2% Score 194; DB 6; Length 1469;
 Best Local Similarity 100.0%; Pred. No. 1,90-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 TTTGATTAATGGCTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTTAAGAA 60
 |||||||
 DB 1268 TTTGATTAATGGCTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTTAAGAA 1427
 UY 61 GCTTAACTTTTAAAGCTATGTAATCAATTCATTCATTCATTCATTCATTCATTC 120
 |||||||
 DB 1428 GCTTAACTTTTAAAGCTATGTAATCAATTCATTCATTCATTCATTCATTCATTC 1487

121 AACCTGTTAATTAAGCTGAAATATATAGCTAGATTAATTAAGCAATATTAT 180
|||||
Db 1388 AAGTCTTTAATTAAGCTGAAATATATATAGCTAGATTTAATTAAGCAATATTAT 1447
|||
QY 181 AATAGCAAAATAT 194
|||||
Db 1448 AATAGCAAAATAT 1461

RESULT 4
LOCUS HUM1L1 1496 bp mRNA linear PRI 11-JUN-1993
DEFINITION Human monocyte interleukin 1 (IL-1) mRNA, complete cds.
ACCESSION K02770
VERSION K02770.1 GI:186268
KEYWORDS Interleukin; interleukin 1.
SOURCE Human endotoxin-stimulated monocyte, cDNA to mRNA, clones pA-26,
pCD-415 and pCD-1218.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1496)
Auron, P.E., Webb, A.C., Rosenwasser, L.J., Mucci, S.F., Rich, A.,
Wolff, S.M. and Dinarello, C.A.
Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7907-7911 (1984)
JOURNAL MEDLINE
PUBMED 6083965

COMMENT A potential poly-A signal is found at position 1484-1489. Two
basic sequences that could be sites for protein processing, similar
to those observed for peptide hormones, are found at positions
708-715 and 723-728.

FEATURES
source location/Qualifiers
1..1496
/organism="Homo sapiens"
/db_xref="taxon:9606"
c1..1496
/product="IL-1 mRNA"
87..896
/note="Interleukin 1 precursor polypeptide"
/codon_start=1
/protein_id="AAA36106.1"
/db_xref="GI:307043"

CDS
mRNA
87..896
/product="IL-1 mRNA"

BASE COUNT 416 a 361 c 328 g 391 t
ORIGIN 104 bp upstream of A1ul site.

Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
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Db 1269 TTTTGATTCATGGCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTTAAGA 1328

QY 61 GGCCTTTTAAATAGCTAGCAATCAATTTGGAGTGGTCTCTTTAATC 120
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Db 1329 GGCCTTTTAAATAGCTAGCAATCAATTTGGAGTGGTCTCTTTAATC 1388

QY 121 AAGCTTTTAATTAAGCTGAAATATATATAGCTAGATTAATTAAGCAATATTAT 180
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Db 1389 AAGCTTTTAATTAAGCTGAAATATATATAGCTAGATTAATTAAGCAATATTAT 1448

QY 181 AATAGCAAAATAT 194
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Db 1449 AATAGCAAAATAT 1462

RESULT 5

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LOCUS HUM1L1C 1496 bp mRNA linear PRI 06-JAN-1995
DEFINITION Human monocyte interleukin mRNA, complete cds.
ACCESSION M54933.1 M38756
VERSION M54933.1 GI:186287
KEYWORDS Interleukin 1.
SOURCE Human monocyte, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1496)
Webb, A.C., Dinarello, C.A., Rosenwasser, L.J., Mucci, S.F., Rich, A.,
Wolff, S.M. and Auron, P.E.
Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
Adv. Gene Technol. 22, 339-340 (1985)
JOURNAL MEDLINE
PUBMED 8811114

FEATURES
source location/Qualifiers
1..1496
/organism="Homo sapiens"
/db_xref="taxon:9606"
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88..897
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BASE COUNT 416 a 367 c 322 g 391 t
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QY 61 GGCCTTTTAAATAGCTAGCAATCAATTTGGAGTGGTCTCTTTAATC 120
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QY 121 AAGCTTTTAATTAAGCTGAAATATATATAGCTAGATTAATTAAGCAATATTAT 180
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QY 181 AATAGCAAAATAT 194
|||||
Db 1449 AATAGCAAAATAT 1462

RESULT 6
LOCUS F00846 1507 bp RNA linear PRI 29-SEP-1997
DEFINITION cDNA sequence for human IL-1.
ACCESSION F00846
VERSION F00846.1 GI:2169107
KEYWORDS JP 1986119191-A/1.
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1507)
 AUTHORS FOLLETSPOUL, A., CHIVAKARU, E.D., ANDOTIYU, S.J., AREKISANDU, R.,
 SHIVAKUMAR, E.D., KUTTY, and RANIL, J.K.
 TITLE HUMAN IL-10 RNA HAVING BIOLOGICALLY ACTIVE HUMAN IL-1 PROTEINCODE
 JOURNAL J. J. 1961, 1991, A 1 00-108-1986
 MASSACHUSETTS INST OF TECHNOLOGY, NEW INSRAND MEDICAL CENTER
 BOSTON, MA 02120, U.S.A., TRINITECH ORO TAPUSO KARETSOULI, DEFESEURE
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 COMMENT
 05 Human (homo sapiens)
 EN JP 196119191 A/1
 06 JUN-1986
 07 18 MAY-1985 JP 1985104978
 08 MAY-1984 US 84 611669, 11-FEB-1985 US 85 700374 P1
 09 FILIPINOS 11 AUBIN, CHIVAKARU EE DEINABERO, P1 ANDOTIYU SHIL
 10 80,
 11 AREKISANDU, RITSCH, SHIVAKUMAR EMO DOKUPU, RIL CHERUKU, P1
 12 JEE ROZENWASSER
 13 C12N15/00, A61K 39/495, C07K 14/00, C12N1/00, C12N5/00, C12P21/02, PC
 (C12N1/00)
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 16 topology: linear;
 17 byproduct: No;
 18 source: No;
 19 *source: tissue: lymph. blood;
 20 *source: cell: type: monocyte;
 21 key location/Qualifiers
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 24 3'UTR 897..898
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 26 mat_peptide 711..893 /product: 'peptide with human IL-1 activity' FT
 27 4'UTR 894..1507 /product: 'peptide with human IL-1 activity' FT
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 29 1..1507
 30 /organism: "Homo sapiens"
 31 /db_xref: "taxon:32644"
 32 BASE COUNT 427 a 361 c 328 g 391 t
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 34 Query Match 82.2% Score 194; DB 6; Length 1507;
 35 Best local similarity 100.0%; Prod. No. 1.6e-86;
 36 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 AATCTCTTAATTAAGACTGAAATATATAGCTCAGATTATTAAATGCAATTTAT 180
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Db 8830 AACTGCTTTTAATTAAGACTGAAATATATAGCTCAGATTATTAAATGCAATTTAT 8889
QY 181 AATGAGCAAAATAT 194
|||||
Db 8890 AATGAGCAAAATAT 8903

RESULT 9
AX067266 9721 bp DNA linear PAT 24-JAN-2001
LOCUS Sequence 1 from Patent WO0100880.
ACCESSION AX067266
VERSION AX067266.1 GI:12544890
KEYWORDS
SOURCE Human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Moleleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 9721)
Patt,G.W., Cox,A., Camp,N.J. and di Giovine,F.S.
Diagnostics and therapeutics for diseases associated with an 11-1
inflammatory haplotype
Patent: WO 0100880-A 2 04-JAN-2001;
JOURNAL Interleukin Genetics, Inc. (US)
FEATURES
Source 1..9721
Location/Qualifiers
BAC COUNT 2661 a 2328 c 2122 g 2608 t 2 others
ORIGIN
Query Match 82.2%; Score 194; DB 6; Length 9721;
Best local similarity 100.0%; Pred. No. 1,2e-86;
Matches 194: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCATTCATTCGCTTAATTTATTCAGAGGGGCAAGAGTACAGAGTGTCTTAAAGA 60
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Db 8710 TTTCATTCATTCGCTTAATTTATTCAGAGGGGCAAGAGTACAGAGTGTCTTAAAGA 8769
QY 61 GCTTACTTTTAAATGAGTAAATTTCAATTTGAGTGTGTCTCTTTAAATC 120
|||||
Db 8770 GCTTACTTTTAAATGAGTAAATTTCAATTTGAGTGTGTCTCTTTAAATC 8829
QY 121 AAGTCTTTAAATGAGTAAATTTCAATTTGAGTGTGTCTCTTTAAATC 180
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Db 8830 AAGTCTTTAAATGAGTAAATTTCAATTTGAGTGTGTCTCTTTAAATC 8889
QY 181 AATGAGCAAAATAT 194
|||||
Db 8890 AATGAGCAAAATAT 8903

RESULT 10
AX469435 9721 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 1 from Patent WO0222877.
ACCESSION AX469435
VERSION AX469435.1 GI:21901721
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1
Hill,J.A., Wang,Z.C., Anderson,D.J. and Yunus,E.J.
Variants of 11-1 beta gene and cdk6 gene for diagnosing unexplained
recurrent pregnancy loss
Patent: WO 0222877-A 1 21-MAR-2002;
JOURNAL THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) : LANA-FARRER CANCER

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INSTITUTE, INC. (US)
FEATURES
Source 1..9721
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2661 a 2328 c 2122 g 2608 t 2 others
ORIGIN
Query Match 82.2%; Score 194; DB 6; Length 9721;
Best local similarity 100.0%; Pred. No. 1,2e-86;
Matches 194: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCATTCATTCGCTTAATTTATTCAGAGGGGCAAGAGTACAGAGTGTCTTAAAGA 60
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Db 8710 TTTCATTCATTCGCTTAATTTATTCAGAGGGGCAAGAGTACAGAGTGTCTTAAAGA 8769
QY 61 GCTTACTTTTAAATGAGTAAATTTCAATTTGAGTGTGTCTCTTTAAATC 120
|||||
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|||||
Db 8830 AAGTCTTTAAATGAGTAAATTTCAATTTGAGTGTGTCTCTTTAAATC 8889
QY 181 AATGAGCAAAATAT 194
|||||
Db 8890 AATGAGCAAAATAT 8903

RESULT 11
HST11B 9721 bp DNA linear PRI 26 JUN 1997
LOCUS Human gene for prointerleukin 1 beta.
ACCESSION X04500.1 GI:33788
VERSION X04500.1 GI:33788
KEYWORDS Interleukin 1 beta.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 9721)
Clark,R.D., Collins,K.L., Gandy,M.S., Webb,A.C. and Auron,P.E.
Genomic sequence for human prointerleukin 1 beta: possible
evolution from a reverse transcribed prointerleukin 1 alpha gene
JOURNAL Nucleic Acids Res. 14 (20): 7897-7914 (1986)
MEDLINE 87040762
PUBMED 3490554
COMMENT Data kindly reviewed (13-MAY-1988) by Clark R.D.
FEATURES
Source 1..9721
Location/Qualifiers
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/mole="Alu repeat"
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/note="TATA-box like sequence"
/CAT_signal 1809..1816
/CAT_signal 1859..1866
/JAT_signal 1903..1909
/prim_transcript 1934..8953
/exon 1934..2005
/misc_feature 2006..2005
/misc_feature complement((1936..1943)
/note="Pol. viral enhancer core sequence"
/intron 2006..2465
/repeat_region 2039..2055
/misc_feature 2291..2297
/note="Pol. viral enhancer core sequence"

```


Tomakin, I. B., Emel'yanov, A. V., Kozlov, A. P., Korusova, V. G.,
Kotlov, A. Y., Kurbatova, T. V., Reshetnikov, V. L., Simbirskiy, A. S.,
Kellinskii, S. A. and Violetskiy, Y. P.
Cloning of the cDNA coding for human proinfectin-1 alpha and
proinfectin-1 beta

JOURNAL
MEDLINE
90245285
PubMed
2635664

FEATURES
Source location/Qualifiers

1..1473
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SFVQGFESNDKIPIVAILGLKFNKLISVCLKDKDPTQLFESVDPKPKMKKEPVFN
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58..864
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/gene="proil-1 beta"
/product="proinfectin-1 beta"

BASE COUNT 408 a 353 c 325 g 387 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.2e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTTAATGGCTGAATTTATTCAGAGGGGGCAAGACTAGAGTCTGTAAAGACGCTA 65
|||||
DB 1242 ATTCATTGGCTGAATTTATTCAGAGGGGGCAAGACTAGAGTCTGTAAAGACGCTA 1301
QY 66 GTTTTAATAGCTATGCAATTCATTTGAGCTGGTGTCTCTTTAATCAAGTC 125
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DB 1302 GTTTTAATAGCTATGCAATTCATTTGAGCTGGTGTCTCTTTAATCAAGTC 1361
QY 126 CTTTAATTAAGCTAGAAATATATTAAGCTAGATTTAATGAAGATTTTAAATG 185
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DB 1362 CTTTAATTAAGCTAGAAATATATTAAGCTAGATTTAATGAAGATTTTAAATG 1421
QY 186 AGCAAAATAT 194
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DB 1422 AGCAAAATAT 1430

RESULT 14

LOCUS ARO30386 1497 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 10 from patent US 5861267.

ACCESSION ARO30386

VERSION ARO30386.1 GI:5943600

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 1497)

AUTHORS

TITLE Methods, nucleotide sequences and host cells for assaying exogenous

and endogenous protease activity

Patent: US 5861267-A 10 19-JAN-1999;

FEATURES
Source location/Qualifiers
1..1497

BASE COUNT 411 a 365 c 331 g 390 t
ORIGIN

Query Match 80.1%; Score 189; DB 6; Length 1497;
Best Local Similarity 100.0%; Pred. No. 5.2e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 66 GTTTTAATAGCTATGCAATTCATTTGAGCTGGTGTCTCTTTAATCAAGTC 125
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DB 1331 GTTTTAATAGCTATGCAATTCATTTGAGCTGGTGTCTCTTTAATCAAGTC 1390
QY 126 CTTTAATTAAGCTAGAAATATATTAAGCTAGATTTAATGAAGATTTTAAATG 185
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QY 186 AGCAAAATAT 194
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DB 1451 AGCAAAATAT 1459

RESULT 15

LOCUS E06734 1497 bp RNA linear PAT 29-SEP-1997

DEFINITION DNA encoding H-1 beta.

ACCESSION E06734

VERSION E06734.1 GI:2174916

KEYWORDS JP 1994041185-A/5.

SOURCE Unidentified.

ORGANISM synthetic construct.

artificial sequences.

REFERENCE 1 (bases 1 to 1497)

AUTHORS Hioaki, M., Shoji, Y. and Mizushima, Y.

TITLE OHOSPHOLIGONUCLEOTIDE AND ITS USE

JOURNAL Patent: JP 1994041185-A 5 15-FEB-1994;

COMMENT 1. T. T. KENRYUSHO: RK

PN JP 1994041185-A/5

PD 15-FEB-1994

PE 16-JUL-1992 JP 1992213519

PT HITAKI MEGUMI, SHOOT YOKO, MIZUSHIMA YUTAKA

PC C07H21/04, A61K31/70, A61K31/70, C12P19/14;

CC strandedness: double;

CC topology: linear;

CC key Location/Qualifiers

FT mat_peptide 1..1497

FT /product="H-1 beta".

FEATURES
Source location/Qualifiers
1..1497

BASE COUNT 411 a 365 c 331 g 390 t

ORIGIN

Query Match 80.1%; Score 189; DB 6; Length 1497;

Best Local Similarity 100.0%; Pred. No. 5.2e-84;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATGGCTGAATTTATTCAGAGGGGGCAAGACTAGAGTCTGTAAAGACGCTA 65
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QY 66 GTTTTAATAGCTATGCAATTCATTTGAGCTGGTGTCTCTTTAATCAAGTC 125
|||||
DB 1331 GTTTTAATAGCTATGCAATTCATTTGAGCTGGTGTCTCTTTAATCAAGTC 1390
QY 126 CTTTAATTAAGCTAGAAATATATTAAGCTAGATTTAATGAAGATTTTAAATG 185
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Tue Mar 18 16:20:48 2003

us-09-247-874c-2_copy_8710_8945.oli.rge

Page 8

QY 186 ACZAAATAT 194
|||||
DB 1451 ACZAAATAT 1459

Search completed: March 17, 2003, 21:05:14
Job Time: 1157 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1994 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 17:37:19 ; Search time 224 Seconds
(without alignments)
2172.641 Million cell updates/sec

Title: US-09-247-874C-2_COPY_8710_8945

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	236	100.0	9721	21	AAA50175 Human interleukin-
2	234.4	99.3	9721	20	AAE75924 Human interleukin-
3	234.4	99.3	9721	21	AAE20945 Human interleukin-
4	234.4	99.3	9721	21	AAE63768 Human IL-1B gene.
5	234.4	99.3	9721	21	AAA50174 Human interleukin-
6	234.4	99.3	9721	21	AAA34823 Human adenosine re
7	234.4	99.3	9721	22	AAE27666 IL-1B DNA. Uniden
8	234.4	99.3	9721	22	AAE91434 Human IL-1B nucleo
9	234.4	99.3	9721	24	AAE35192 Human prointerleuk

10	234.4	99.3	29433	21	AAE20950 Human interleukin-
11	234.4	99.3	29433	21	AAA48428 Human adenosine re
12	234.4	99.3	209273	21	AAE21417 Human factor-relat
13	231.8	98.2	7824	16	AAO74052 Human interleukin-
14	231.8	98.2	7824	22	AAH24368 Human IL-1B gene.
15	231.8	98.2	14690	20	AAE22403 Human IL-1B gene
16	230.2	97.5	7824	24	ABK50291 Human interleukin
17	230.2	97.5	7824	24	ABK50293 Human interleukin
18	229.6	97.3	1507	6	AAE50060 Sequence encoding
19	229.6	97.3	1507	14	AAE50981 Human interleukin-
20	229.6	95.9	1404	7	AAE60283 Sequence encoding
21	226.4	95.9	1404	8	AAE70505 Sequence encoding
22	226.4	95.9	1404	14	AAO51110 Human interleukin-
23	226.2	95.8	1497	21	AAE20944 Human interleukin-
24	226.2	95.8	1497	21	AAE44822 Human adenosine re
25	226.2	95.8	1497	24	ABK81933 Human cDNA differe
26	224.8	95.3	656	21	AAE51659 Human interleukin-1
27	224.8	95.3	1496	21	AAE20946 Human interleukin-
28	224.8	95.3	1496	21	AAA44824 Human adenosine re
29	224.6	95.2	1497	15	AAE58462 IL-1 beta gene.
30	205.8	87.2	1514	21	AAE55973 cDNA encoding huma
31	200.8	85.1	1382	24	AAE46348 Human interleukin-
32	195	82.6	454	16	AAT20507 Human gene simarti
33	170	72.0	8639	20	AAE02995 Human IL-1B gene
34	163	69.1	1458	11	AAE05591 Monkey IL-2 beta g
35	119.6	50.7	1429	13	AAE02825 Sequence encoding
36	91	38.6	8760	15	AAE74473 Interleukin-10
37	70.6	29.5	1750	9	AAE80433 Bayle interleukin
38	69.2	29.3	1322	10	AAE90914 Rat IL-1B gene.
39	69.2	29.3	1327	14	AAE94458 Rat IL-1B gene.
40	67.4	28.6	1329	24	ABE63523 Rat sequence diffe
41	60	25.4	1330	24	ABE63523 Mouse IL-1. Mus m
42	58.4	24.7	60	24	AAE40567 Human splid tran
43	58.4	24.7	1339	21	AAE94191 Mouse interleukin-
44	44	18.6	44	21	AAA50182 Probe used to dete
45	44	18.6	44	21	AAA50184 Probe used to dete

ALIGNMENTS

RESULT 1	AAA50175	Standard: DNA: 9721 BP.
ID	AAA50175	Standard: DNA: 9721 BP.
AC	AAA50175:	
DT	07-NOV-2000	(first entry)
XX	Human interleukin-1 beta allele 2 (c6912).	
DE	Human interleukin-1 beta; IL-1B; human; polymorphism; inflammation;	
XX	interleukin-1 beta; IL-1B; human; polymorphism; inflammation;	
XX	coronary artery disease; osteoporosis; nephropathy;	
KW	alopecia areata; Graves disease; systemic lupus erythematosus;	
KW	lichen sclerosis; ulcerative colitis; diabetic retinopathy;	
KW	periodontal disease; juvenile chronic arthritis; psoriasis;	
KW	insulin dependent diabetes; asthma; lung fibrosis;	
KW	chronic inflammatory liver disease; rheumatoid arthritis;	
KW	chronic inflammatory lung disease; anti-inflammatory; osteoporosis;	
KW	dermatological; immunosuppressive; antidiabetic; antithyroid;	
KW	antiarrhythmic; antineoplastic; antistomatitis; antipsoriasis;	
KW	hepatotropic; antitumor; antidiabetic; therapy; ds.	
OS	Human sapiens.	
XX		
XX	key	Location/Qualifiers
XX	variation	replace(8904,C)
XX		/tag a
XX		/note- "IL-1B allele 2 (c6912)"
XX	W0200047619-AL.	
XX	17-MUG-2000.	
PD		

RESULT 3
 ID AAF20945 standard; DNA: 9721 BP.
 AC AAF20945:
 DT 14-MAR-2001 (first entry)
 XX Human interleukin-1 polynucleotide fragment #2512.
 DE
 KW low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosolic;
 KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; SS.
 KW
 OS Homo sapiens.
 PN M0200062736-7A2.
 XX
 XX 26-OCT-2000.
 PD
 PE 24-MAR-2000; 2000WO-0508020.
 XX
 XX 06-APR-1999; 9905-0127958.
 PR
 XX
 PA (U99C-) UNIV EAST CAROLINA
 PA (NYCE/) NYCE J W.
 XX
 P1 Nyce JW:
 XX
 DR WPI: 2000-679539/66.
 PT
 P1 Low adenosine (A) content antisense oligonucleotides which do not
 P1 trigger adenosine receptors during metabolism, useful e.g. for treating
 P1 cancers and respiratory obstructions -
 XX
 XX
 PS Disclosure; page 230-232; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytosolic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.

XX	Sequence	9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other.
XX	Query Match	99.3%; Score 234.4; Dh 21; Length 9721;
XX	Best Local Similarity	99.6%; Pred. No. 2,6e-45;
XX	Matches 235; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
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Db	8710	TTTTATTCATCTGCTCTATTATTTCGAAGGGGCGACAGAGTAGTGCTGTGAAGA 8769
QY	61	GCTGTGTTTAAATAGCATGGAATCATTCATTTTGGACGGTGTCTCTTAAATC 120
Db	8770	GCTTGAGTTTAAATAGCATGGAATCATTCATTTTGGACGGTGTCTCTTAAATC 8829
QY	121	AAGTCTTAAATTAAGTCTGAAAATATTAACCTGACATTAATTAAGGGAAATATTA 180
Db	8830	AAGTCTTAAATTAAGTCTGAAAATATTAACCTGACATTAATTAAGGGAAATATTA 8884
QY	181	AAATGACCAATATCATCTGTTCAATGCTGTGAAATAAATCTGACTGAAGAAAA 236
Db	8890	AAATGACCAAAATCATCTGTTCAATCTCTGAAATAAATCTGACTGAAGAAAA 8945
XX	RESULT 4	
XX	AA653768	
XX	AA63768 standard; DNA: 9721 BP.	
XX	AA63768;	
XX	08-FEB-2001 (first entry)	
XX	Human IL-1B gene.	
XX	Human: IL-1B; interleukin-1B; cytosolic; antiinflammatory;	
XX	Immunosuppressive; dermatological; antimicrobial; antiarthritic;	
XX	IL-1 receptor antagonist; tumor necrosis factor alpha antagonist	
XX	rheumatoid lung disease; interstitial pneumonia; pulmonary fibrosis;	
XX	rheumatoid arthritis; systemic lupus erythematosus; Sjogren's syndrome;	
XX	systemic sclerosis; dermatomyositis; chromosome 2; ds.	
XX	Homo sapiens.	
XX	FN	
XX	W0200060117-A2.	
XX	12-OCT-2000.	
XX	1-MAR-2000; 2000WO-0508492.	
XX	02-APR-1999; 99US-0286108.	
XX	(INTE-) INTERLEUKIN GENETICS INC.	
XX	Duff GW, Di Giovanni FS, Whyte M;	
XX	WPI: 2000-656234/63.	
XX	Method for predicting the risk of interstitial lung disease, comprising	
XX	detecting an interleukin-1 receptor antagonist allele and tumor	
XX	necrosis alpha allele or an allele in linkage disequilibrium with	
XX	either of these alleles -	
XX	Claim 6; Fig 2; 102pp; English.	
XX	The present sequence is provided in a specification relative to a method	
XX	for determining whether a subject has or is predisposed to develop an	
XX	interstitial lung disease. The method involves detecting an interleukin-1	
XX	receptor antagonist (IL-1R) (-2018) allele 2, a tumor necrosis alpha	
XX	(TNF-A) (-308) allele 2, or an allele in linkage disequilibrium with	
XX	either of these two alleles. The method may be used to determine whether	
XX	a subject has or is predisposed to develop an interstitial pneumonia or a	
XX	pulmonary fibrosis and other disorders such as rheumatoid arthritis,	
XX	systemic lupus erythematosus, Sjogren's syndrome, systemic sclerosis.	

PN WO200009525-A2.
 XX 24-FEB-2000.
 XX 03-AUG-1999; 99WO-US17712.
 XX 03-AUG-1998; 98US-005212.
 XX (UYEC-) UNIV EAST CAROLINA.
 PA NYCE JW;
 XX WPI: 2000-205971/18.
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 XX Disclosure: Page 673-675; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antitasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects affect the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA3213 to AAA3512 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure or the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.
 XX
 XX
 SO Sequence 9721 BP: 2661 A; 2328 C; 2122 G; 2608 T; 2 other:
 Query Match 99.3%; Score 234.4; DB 21; Length 9721;
 Best Local Similarity 99.6%; Pred. No. 2,66-45;
 Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTTGATTCATGCGCTAATTATTCAGAGGGGCGAAGAGTAGGAGTGTCTTAAGA 60
 DB 8710 TTTGATTCATGCGCTAATTATTCAGAGGGGCGAAGAGTAGGAGTGTCTTAAGA 8769
 QY 61 GCGTACGTTTAAATAGCTATGGAATCAATTCATTGGAGTGGTGGCTCTTTAAATC 120
 DB 8770 GCGTACGTTTAAATAGCTATGGAATCAATTCATTGGAGTGGTGGCTCTTTAAATC 8829
 QY 121 AAGTCTTTAATTAAGACAGCAAAATATATAGCTACAGATTTATTAATGGCAATTTAT 180
 DB 8830 AAGTCTTTAATTAAGACAGCAAAATATATAGCTACAGATTTATTAATGGCAATTTAT 8889
 QY 181 AATAGCAAAATATATATATGTTCAATGTTGCAATTAAGTTCAGCAAGAAAA 236
 DB 8890 AATAGCAAAATATATATATGTTCAATGTTGCAATTAAGTTCAGCAAGAAAA 8945

XX
 AC AAF27666;
 XX 02-APR-2001 (first entry)
 DT
 XX II-1B DNA.
 DE
 XX IL-1; interleukin; inflammation; infection; ds
 XX unidentified.
 OS
 XX W0200100880-A2.
 XX
 XX 04-JAN-2001.
 XX
 XX 30-JUN-2000; 2000WO-US18318.
 XX
 XX 30-JUN-1999; 99US-0145217.
 XX
 XX (INTE-) INTERLEUKIN GENETICS INC.
 XX
 XX DUFF GW, COX A, CAMP NJ, DI GIOVINE FS;
 P1 WPI: 2001-102903/11.
 XX
 XX Determining whether a subject has or is predisposed to disease
 PT associated with IL-1 polymorphism involves determining presence of
 PT marker or allele comprising IL-1 inflammatory haplotype -
 XX
 XX Disclosure: Fig 4; 84pp; English.
 XX
 CC The present invention relates to a new method for determining whether
 CC a subject has or is predisposed to developing a disease or condition
 CC that is associated with an IL (interleukin)-1 inflammatory haplotype,
 CC comprises detecting at least one allele of the haplotype, where the
 CC presence of the allele indicates that the subject is predisposed to
 CC the development or has the disease or condition.
 CC The method is useful for determining whether a subject has or is
 CC predisposed to inflammatory disease, a degenerative disease, an
 CC immunological disorder, an infectious disease, trauma induced disease,
 CC or cancer. The above conditions associated with an IL-1 inflammatory
 CC haplotype can be treated or prevented by administering a therapeutic
 CC that compensates for a causative mutation that is in linkage
 CC disequilibrium with at least one IL-1 polymorphism.
 CC
 XX
 XX
 SO Sequence 9721 BP: 2661 A; 2328 C; 2122 G; 2607 T; 3 other:
 Query Match 99.3%; Score 234.4; DB 22; Length 9721;
 Best Local Similarity 99.6%; Pred. No. 2,66-45;
 Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTTGATTCATGCGCTAATTATTCAGAGGGGCGAAGAGTAGGAGTGTCTTAAGA 60
 DB 8710 TTTGATTCATGCGCTAATTATTCAGAGGGGCGAAGAGTAGGAGTGTCTTAAGA 8769
 QY 61 GCGTACGTTTAAATAGCTATGGAATCAATTCATTGGAGTGGTGGCTCTTTAAATC 120
 DB 8770 GCGTACGTTTAAATAGCTATGGAATCAATTCATTGGAGTGGTGGCTCTTTAAATC 8829
 QY 121 AAGTCTTTAATTAAGACAGCAAAATATATAGCTACAGATTTATTAATGGCAATTTAT 180
 DB 8830 AAGTCTTTAATTAAGACAGCAAAATATATAGCTACAGATTTATTAATGGCAATTTAT 8889
 QY 181 AATAGCAAAATATATATATGTTCAATGTTGCAATTAAGTTCAGCAAGAAAA 236
 DB 8890 AATAGCAAAATATATATATGTTCAATGTTGCAATTAAGTTCAGCAAGAAAA 8945

RESULT 7
 AAF27666
 ID AAF27666 standard; DNA: 9721 BP.

RESULT 8
 AAC91434
 ID AAC91434 standard; DNA: 9721 BP.

DT 14-MAR-2001 (first entry)
 XX
 DE Human interleukin-1 polynucleotide fragment #2517.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiallergic; analgesic; hypotensive; cytosolic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200062746-A2.
 XX
 PD 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-0508020.
 XX
 XX 06-APR-1999; 990S-0127958.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 XX (NYEC/) NYEC J W.
 XX
 XX NYEC JW:
 XX
 DR WPI: 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions.
 XX
 PS Disclosure: Page 221-227; 1592pp: English.
 XX
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (1) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiallergic, hypotensive and cytosolic activities.
 CC The antisense oligonucleotides and (1) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergies
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SO Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 2 other.
 Query Match 99.38; Score 234.4; DB 21; Length 29433;
 Best Local Similarity 99.68; Pred. No. 3e-45;
 Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTGATTCATTCGCTAAATTAATCAAGAGGGGCAAGAGAGTGTCTGTAATAA 60
 DB 22177 TTTTCATTCATTCGCTAAATTAATTAAGAGGGGCAAGAGAGTGTCTGTAATAA 22236
 QY 61 GCGTACTTTTAAAGCTAATGGAATCAATTCATTCATTCATTCATTCATTCATTC 120
 DB 22237 GCGTACTTTTAAAGCTAATGGAATCAATTCATTCATTCATTCATTCATTCATTC 22296
 QY 121 AAGCTTTTAATTAAGACAGCAAAATATATAAGCTAGATTAATTAATAGGCAATATTA 180
 DB 22297 AAGCTTTTAATTAAGCTAATGGAATCAATTCATTCATTCATTCATTCATTCATTC 22356
 QY 181 AAGTGAAGCAATATGATACGCTTCAATGCTGCAAAATATATTCATTCGAGCAAAA 236
 DB 22357 AAGTGAAGCAATATGATACGCTTCAATGCTGCAAAATATATTCATTCGAGCAAAA 22412
 RESULT 11
 AAA34828
 ID AAA34828 standard; DNA; 29433 BP.
 AC AAA34828:
 XX
 XX 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2517.
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiallergic; cytosolic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-0517712.
 XX
 XX 03-AUG-1999; 980S-0095212.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 XX
 XX NYEC JW:
 XX
 DR WPI: 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischaemia or
 PT cancers.
 XX
 PS Disclosure: Page 677-684; 1343pp: English.
 XX
 XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiallergic, cytosolic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including


```

XX XX Key Location/Qualifiers
FH misc_difference 1331
FT /tag- a
FT /note= "N is undefined"
XX XX
XX JF07123984-A.
XX
XX 16-MAY-1995.
XX
XX 05-NOV-1993; 93JP-0275852.
XX
XX 05-NOV-1993; 93JP-0275852.
XX
XX (HITB ) HITACHI CHEM CO LTD.
XX
XX WPI: 1995-211627/28.
XX
XX A primer for the detection and the determ. of a specific messenger
PT RNA - can detect and determine specific mRNA(s) with high
PT reliability
XX
XX Example 18; page 17-20; 35pp; Japanese.
XX
XX AA074052 is interleukin-1-beta cDNA and AA074019-21 are primers used for
CC the amplification of this cDNA. They are used specifically for the
CC detection and isolation of this sequence. The primers have the
CC advantage of high sensitivity and reliability and are useful in the
CC pharmaceutical industry.
XX
XX Sequence 7824 BP; 2099 A; 1905 C; 1624 G; 2195 T; 1 other:
SQ
Query Match 98.2%; Score 231.8; DB 16; Length 7824;
Best Local Similarity 99.1%; Pred. No. 1e-44;
Matches 233; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
UY 2 TTGATTCATGCTGCTAATTATTTCACAGGGGCAAGAAATGACAGTGTCTGTAAGAAG 61
DB 7153 TTTTATTCATGCTGCTAATTATTTCACAGGGGCAAGAAATGACAGTGTCTGTAAGAAG 7212
UY 62 CTTAGCTTTTAAATACCTATGCAATTCATTTGGACTGTGCTCTCTTTAATCA 121
DB 7213 CTTAGCTTTTAAATACCTATGCAATTCATTTGGACTGTGCTCTCTTTAATCA 7272
UY 122 AGTCCTTTAATAGAGCTGAATATATTAAGCTACATATTTAATGGAATATTATA 181
DB 7273 AGTCCTTTAATAGAGCTGAATATATTAAGCTACATATTTAATGGAATATTATA 7332
UY 182 AATGAGCAATATGATAGTGTCTGCAATGCTCTGCAATTAAGCTCTGCTGAAGAAA 236
DB 7333 AATGAGCAATATGATAGTGTCTGCAATGCTCTGCAATTAAGCTCTGCTGAAGAAA 7387

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FT variation replace(346,T)
FT /tag- b
FT /standard_name= "Single nucleotide polymorphism"
FT 924..970
FT /tag- c
FT /number= 2
FT 1536..1587
FT /tag- d
FT /number= 3
FT 3576..3777
FT /tag- e
FT /number= 4
FT replace(4258,A)
FT /tag- f
FT /standard_name= "Single nucleotide polymorphism"
FT replace(4336,T)
FT /tag- g
FT /standard_name= "Single nucleotide polymorphism"
FT 4323..4487
FT /tag- h
FT /number= 5
FT 5723..5853
FT /tag- i
FT /number= 6
FT replace(6421,G)
FT /tag- j
FT /standard_name= "Single nucleotide polymorphism"
FT 6570..6782
FT /tag- k
FT /number= 7
FT replace(6883,A)
FT /tag- l
FT /standard_name= "Single nucleotide polymorphism"
FT 7020121639-A1.
FT 29-MAR-2001.
FT 20-SEP-2000; 2000WO-0525794.
FT 22-SEP-1999; 99US-0155412.
FT (GENA-) GENAISSANCE PHARM INC.
FT Chew A, Choi J, Denton RR, Nandabalan K, Stephens JC;
FT WPI: 2001-389617/41.
FT New polynucleotide useful for therapeutic purposes, comprises
FT nucleotide polymorphisms of Interleukin-1b gene
FT Claim 1; Fig 1; 57pp; English.
XX
XX The present invention relates to an isolated polynucleotide comprising
XX a nucleotide sequence which is a polymorphic variant of the fully
XX defined 7821 base pair Interleukin-1 beta (IL1B) gene reference
XX sequence given in the specification or its fragment or complement.
XX CC The IL1B gene polymorphic variant is useful for therapeutic purposes
XX for studying the expression and biological function of IL1B, for
XX developing drugs targeting this protein, and in diagnostics and
XX forensic applications. The method is useful for developing tests and
XX therapeutic treatments for inflammatory and immune disorders. The
XX present sequence is the 7821 bp IL1B gene reference sequence.
XX
XX Sequence 7824 BP; 2099 A; 1905 C; 1624 G; 2195 T; 1 other:
SQ
Query Match 98.2%; Score 231.8; DB 22; Length 7824;
Best Local Similarity 99.1%; Pred. No. 1e-44;
Matches 233; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
UY 2 TTGATTCATGCTGCTAATTATTTCACAGGGGCAAGAAATGACAGTGTCTGTAAGAAG 61
DB 7153 TTTTATTCATGCTGCTAATTATTTCACAGGGGCAAGAAATGACAGTGTCTGTAAGAAG 7212

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GenCode version 5.1.4-p5.4578
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OM nucleic acid search, using sw model

Run on: March 17, 2003, 17:38:45 : Search time 1149 Seconds

(without alignments)
5977.600 Million cell updates/sec

Title: US-09-247-874c-2_COPY_8710_8945

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Scoring table:
Gapop 10.0 / Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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2: qb.hq.*
3: qb.in.*
4: qb.om.*
5: qb.ov.*
6: qb.pat.*
7: qb.ph.*
8: qb.pl.*
9: qb.pr.*
10: qb.ro.*
11: qb.sts.*
12: qb.sy.*
13: qb.un.*
14: qb.vl.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vl.*
30: em.hq.hum.*
31: em.hq.in.*
32: em.hq.other.*
33: em.hq.mus.*
34: em.hq.ph.*
35: em.hq.ro.*
36: em.hq.ham.*
37: em.hq.vrt.*
38: em.sy.*
39: em.hqgo.hum.*
40: em.hqgo.mus.*
41: em.hqgo.other.*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
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2	234.4	99.3	9721	6 AX052806	AX052806 Sequence
3	234.4	99.3	9721	6 AX067266	AX067266 Sequence
4	234.4	99.3	9721	6 AX469435	AX469435 Sequence
5	234.4	99.3	9721	6 BS111B	BS111B Sequence
6	231.8	98.2	7824	9 HUM111B	HUM111B Sequence
7	231.8	98.2	17447	9 AT137079	AT137079 Homo sapi
8	231.8	98.2	154214	9 AC079753	AC079753 Homo sapi
9	230.2	97.5	1473	9 HSPK011B	HSPK011B Homo sapi
10	230.2	97.5	1522	9 BC008678	BC008678 Homo sapi
11	229.6	97.3	1507	6 E00846	E00846 cDNA sequen
12	229.6	97.3	1507	6 I07942	I07942 Sequence 1
13	226.4	95.9	1404	6 A21148	A21148 psf, alpha
14	226.4	95.9	1404	6 E01230	E01230 cDNA encodi
15	226.4	95.9	1404	6 E11934	E11934 cDNA encodi
16	226.4	95.9	1404	6 E12090	E12090 Human cDNA
17	226.4	95.9	1404	6 I00228	I00228 Sequence 2
18	226.2	95.8	1497	6 AR030586	AR030586 Sequence
19	226.2	95.8	1497	6 E06734	E06734 DNA encodin
20	226.2	95.8	1497	6 HUM111B	HUM111B Human inte
21	224.8	95.3	656	6 AX027920	AX027920 Sequence
22	224.8	95.3	1496	9 HUM111	HUM111 Human monon
23	224.8	95.3	1496	9 HUM111C	HUM111C Human monon
24	205.8	87.2	1514	6 AR086559	AR086559 Sequence
25	205.8	87.2	1514	6 I00729	I00729 Sequence 2
26	200.8	85.1	1382	6 AX419478	AX419478 Sequence
27	200.4	84.9	1462	6 I01156	I01156 Sequence 1
28	163	69.1	1458	6 E02498	E02498 cDNA encodi
29	136.6	51.9	1476	4 E0320322	E0320322 Delphinap
30	122.4	51.9	1473	4 E092481	E092481 Equus cabal
31	119.6	50.7	1429	6 A19155	A19155 ovine 11-1
32	91	38.6	8760	4 SSPIN11B	SSPIN11B Sus scrofa de
33	89.6	38.0	1458	4 PIGPILKN1B	PIGPILKN1B Sus scrofa
34	76	32.2	1437	10 AEL19622	AEL19622 Cavia por
35	70.6	29.9	1736	4 HOV11B	HOV11B Hovine inte
36	70.6	29.9	1750	6 I03510	I03510 Sequence 1
37	69.2	29.3	1327	6 E01884	E01884 DNA Sequence
38	69.2	29.3	1327	6 E05490	E05490 cDNA encodi
39	67.4	28.6	1329	6 AX401754	AX401754 Sequence
40	67.4	28.6	1329	10 RAT111B	RAT111B Rattus nor
41	62.6	26.5	1403	4 R0111B2	R0111B2 Rattus nor
42	60	25.4	1340	6 E04743	E04743 cDNA encodi
43	58.4	24.7	1339	6 E55193	E55193 Interleukin
44	58.4	24.7	1339	10 M05111B	M05111B Mouse inter
45	57	24.2	175022	2 AC103019	AC103019 Rattus no

ALIGNMENTS

RESULT 1
G10509
LOCUS human STS CHUC.UFR_00699_X04500.P37183 clone UFR_00699_X04500,
DEFINITION sequence tagged site.
ACCESSION G10509.1 G1942358
VERSION G10509.1
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens vector/pUCP1 host-E.coli out-untg+ (CHI108) Marker
Selected genomic DNA prepared from XI individual of French
nationality.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 614)


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DB 8770 GGCACGTTTAAAGTATGACATGATCAATTCAGTTGGACTGCTGCTGCTCCTTAAATC 8829
      |||||||
QY 121 AATGCTTTTAAATAGAGCTGAAAAATATATAGTCAGATTATTTAAATGGAAATATTAT 180
      |||||||
DB 8830 AAGCTCTTTAATTAAGACTGAAAAATATATAGCTCAGATTAATTTAAATGGAAATATTAT 8889
      |||||||
QY 181 AAATGAGCAATATAGATGCTTCATGCTTGCAGAAATTAAGCTCAGTCAAGAGAAA 236
      |||||||
DB 8890 AAATGAGCAATATGATCTACTGTTCAATGGTTTGGAAATTAAGCTCAGTCAAGAGAAA 8945
      |||||||

RESULT 4
AX469435 9721 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 1 from Patent W0222877.
ACCESSION AX469435
VERSION AX469435.1 GI:21901721
KEYWORDS
SOURCE
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hill,J.A., Wang,Z.C., Anderson,D.J. and Yunis,F.J.
TITLE Variants of 11-1 beta gene and cdk6 gene for diagnosing unexplained
JOURNAL recurrent pregnancy loss
PATENT: WO 022877-A 1 21-MAR-2002.
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) : DNA-FARHER CANCER
INSTITUTE, INC. (US)
FEATURES
Source 1.9721
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2661 a 2328 c 2122 g 2608 t 2 others
ORIGIN

Query Match 99.38; Score 234.4; DB 6; Length 9721;
Best Local Similarity 99.68; Pred. No. 1.6e-17;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTGATTCATGCTGCTAATTTATTCAGAGGGGCAAGAGTACGAGTGTCTGTAAAGA 60
      |||||||
DB 8710 TTTGATTCATGCTGCTAATTTATTCAGAGGGGCAAGAGTACGAGTGTCTGTAAAGA 8769
      |||||||
QY 61 GCGTACTTTTAATAGCTATGGAATCAATTCGAGTTGGAGCTGTGCTCTTTTAATC 120
      |||||||
DB 8770 GCGTACTTTTAATAGCTATGGAATCAATTCGAGTTGGAGCTGTGCTCTTTTAATC 8829
      |||||||
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      |||||||
DB 8830 AAGCTCTTTAATAGCTGAAAAATATATAGCTCAGATTATTTAAATGGAAATATTAT 8889
      |||||||
QY 181 AAATGAGCAATATGATGCTTCATGCTTGCAGAAATTAAGCTCAGTCAAGAGAAA 236
      |||||||
DB 8890 AAATGAGCAATATGATGCTTCATGCTTGCAGAAATTAAGCTCAGTCAAGAGAAA 8945
      |||||||

RESULT 5
HSL11B 9721 bp DNA linear PRI 26-JUN-1997
LOCUS Human gene for prointerleukin 1 beta.
ACCESSION X04500
VERSION X04500.1 GI:33788
KEYWORDS Interleukin 1 beta.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Clark,B.D., Collins,K.L., Gandy,M.S., Webb,A.C. and Auron,P.E.
TITLE Genomic sequence for human prointerleukin 1 beta: possible
          evolution from a reverse transcribed prointerleukin 1 alpha gene

```

```

JOURNAL Nucleic Acids Res. 14 (20), 7897-7914 (1986)
MEDLINE 87640762
PUBMED 3490654
COMMENT Date kindly reviewed (13-MAY-1988) by Clark B.D.
FEATURES Location/Qualifiers
Source 1.9721
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="q13-q24"
/clone.lib="leukocyte DNA library"
669..960
/note="Alu repeat"
1576..1581
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1809..1816
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2006..2465
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2039..2055
/note="direct repeat 2"
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SFVQSPHSNDRKPYVALGKRLKLYISCLKDKDKPLQLEFSDPKRKKKEKRVN
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5125..5326
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5327..5873
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5874..6058
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6039..7274
/number=5
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/note="Inverted repeat A"

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OY	62	CCTAGTTTTTAATAGCTAGTGAATCAATTCATTTGGAGCTGGTGGCCGCTTTAAATCA	121
Db	7213	CCTAGTTTTTAATAGCTAGTGAATCAATTCATTTGGAGCTGGTGGCCGCTTTAAATCA	7272
OY	122	AGTCTTTAATTAAGACTGAAAATATATAGCTCAGCATTTATTAATGGGAATATTATA	181
Db	7273	AGTCTTTAATTAAGACTGAAAATATATAGCTCAGCATTTATTAATGGGAATATTATA	7332
OY	182	AATGACATAATATGATCTGTGATGGTGTCAAAATAAACCTCATAGAAGAAA	236
Db	7333	AATGACATAATATGATCTGTGATGGTGTCAAAATAAACCTCATAGAAGAAA	7387
RESULT 7			
LOCUS	AY137079	17447 bp	DNA linear FRI 05-AUG-2002
DEFINITION	Homo sapiens interleukin 1, beta (IL1B) gene, complete cds.		
ACCESSION	AY137079		
VERSION	AY137079.1	GI:22122009	
KEYWORDS	.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 17447) Rieder,M.J., Armet,T.Z., Carrington,D.P., Ozuna,M., Kulaneh,S.A., Rajkumar,N.R., Toib,E.J., Yi,Q. and Nickerson,D.A. Submitted (29-JUL-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA to cite this work please use : SeattleSNPs, NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu). Location/Qualifiers 1..17447 /organism="Homo sapiens" /db_xref="taxon:9606"		
TITLE	JOURNAL.		
COMMENT			
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	/rpl_type=dispersed	/replace="g"	/frequency="0.01"
	302	500..503	3298
	/frequency="0.96"	/replace="t"	/frequency="0.14"
	794	855	2824
	/frequency="0.40"	/replace="a"	/frequency="0.01"
	/replace="t"	3535	3007..3101
	855	/frequency="0.44"	/rpl_family="MIR"
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	/replace="q"	3924..4027	4006
	1274	/gene="IL1B"	/frequency="0.15"
	/frequency="0.40"	/replace="g"	/frequency="0.02"
	/replace="c"	4067..4178	/replace="c"
	1306..8330	/frequency="0.01"	
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	join(1306..1376,1840..1901,2467..2518,4515..4716,		
	5264..5428,6668..6798,7517..8330)		
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	/product="interleukin 1, beta"		
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	6668..6798,7517..7729)		
	/gene="IL1B"		
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Variation	407.0 ⁺ - 407.4 ⁻ /frequncy="0.11B" /frequncy="0.99" /replace="n"
Variation	424.6 ⁺ /frequncy="0.99" /replace="n"
Variation	433.2 ⁺ /frequncy="0.12" /replace="n"
Variation	450.5 ⁺ /frequncy="0.21" /replace="c"
repeat_freqtion	5200 ⁺ /frequncy="0.01" /replace="n"
Variation	5277 ⁺ /frequncy="0.11B" /replace="c"
Variation	5291.6 ⁺ /frequncy="0.03" /replace="n"
Variation	5687.1 ⁺ /frequncy="0.21" /replace="n"
Variation	6334 ⁺ /frequncy="0.11B" /replace="c"
Variation	6874 ⁺ /frequncy="0.01" /replace="n"
Variation	6909.5 ⁺ /frequncy="0.23" /replace="n"
Variation	7114 ⁺ /frequncy="0.15" /replace="n"
Variation	7133 ⁺ /frequncy="0.03" /replace="n"
Variation	7275 ⁺ /frequncy="0.07" /replace="n"
Variation	7277 ⁺ /frequncy="0.01" /replace="n"

Query Match	98.2%	Score 241.8	Pos 92	Length 17447
Blast Local Similarity	99.1%	Pred. No.	4.6e-37	
Motif 244	Conservative	0	Mismatches 2	Tidbits 0
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DB	8100	TTTTATCATCGGTAAFTTAATAAGGAGGAGAAACAAATGACTGTCAAAAATG	8159	
OY	62	CCTACTTTCATAGCTCTGGATTAATTTCTCCATGCTGTCTAAGAACA	121	
DB	8160	CCTACTTTCATAGCTCTGGATTAATTTCTCCATGCTGTCTAAGAACA	8219	
OY	122	AGCTCTTAAATTAATATGAATAATATGAATATGAATATGAATATGAATATGAAT	181	
DB	8220	AGCTCTTAAATTAATATGAATAATATGAATATGAATATGAATATGAATATGAAT	8279	
OY	182	AATGAGCAAAATATCATACTGTCAATGCTTTCTGAATAAACCTGCATGAACAA	246	
DB	8280	AATGAGCAAAATATATATGCTTAATGCTTTCTGAATAAACCTGCATGAACAA	8344	
RESULT 8	AC079753/c			
LOCUS	AC079753	154214 bp	DNA	Linear PRS OL-MAR 2002
DEFINITION	Homo sapiens BAC clone RP116714 from 2, complete sequence.			
VERSION	AC079753.7	G1:14318405		
KEYWORDS	HTG.			
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Cnidaria; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;			
REFERENCE	1 (Jasos 1 to 154214) Stilson,J.E. and Waterston,R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)			
JOURNAL	99063792			
FEATURE	9847174			
REFERENCE	2 (Jasos 1 to 154214) Andrzej,S., Cotton,M., Doubder,A. and Resny,C. The sequence of homo sapiens BAC clone RP116714 Unpublished (2001)			
JOURNAL	3 (Jasos 1 to 154214) Waterston,R.H.			
REFERENCE	Direct Submission Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA			
JOURNAL	5 (Jasos 1 to 154214) Waterston,R.H.			
REFERENCE	Direct Submission Submitted (04-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA			
JOURNAL	6 (Jasos 1 to 154214) Waterston,R.			
REFERENCE	Direct Submission Submitted (09-JAN 2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA			
JOURNAL	7 (Jasos 1 to 154214) Waterston,R.			
REFERENCE	Direct Submission Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA			
JOURNAL	On Jan 6, 2001 This sequence version replaced GI:114029079.			
COMMENT	----- Genome Center			

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 Summary Statistics
 Center Project name: H_NH0067114

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RP11-11 human PAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatematsu, M., Calane, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the right is RP11-725J3. Actual start of this clone is at base position 1 of RP11-67L14; actual end is at base position 154214 of RP11-67L14.

There are polymorphic base differences in the overlap between RP11-67L14 and RP11-725J3.

FEATURES

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 1629..1748
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 11676..11718
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 11687..11996
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 15272..15565
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 18007..18111
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 18112..18406
 /rpt_family="Alu"

SAIHOI, KANEDA MAYUMI, KIKUMOTO YOSHIKAZU, KO HIDEMIITSU, PI KAWAI
 KAZUYOSHI, TAKEKATA SEISUOKO, ISHII KIYOSHI, PI YANAGIHARA YASUO,
 PI HIRAI YOSHIKATSU
 PC C07K14/545.C07H21/04.C12N1/21.C12N5/10.C12N15/09, PC
 C12P21/02//A61K38/00, (C12N1/21.C12R1:19).(C12P21/02.C12R1:19). (C12P21/02.C12R1:91);
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 CC Topology: linear;
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 FI CDS 57..773
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 beta
 FI mat_peptide 312..770
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 ORIGIN

Query Match 95.98; Score 226.4; DB 6; Length 1404;
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 Matches 230; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 DB 1147 TTTTATTCATTTGGTGTATTTATTCGAAGGGGCAAGAGTAGCAGTCTGTAAAGA 1206
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QY 61 GCCTAGTTTTAATAGCTATGCAATTCATTTGGAGTGGTCTGCTGCTTTAATG 120
 |||||||
 DB 1207 GCTTACTTTTATTTAGCTATGCAATTCATTTGGAGTGGTCTGCTGCTTTAATG 1266
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QY 121 AAGTCTTTAATTAAGACTGAAATAVAIAAGCTGCAGATTATTAATGGGATATTAT 180
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 DB 1267 AAGTCTTTAATTAAGACTGAAATAVAIAAGCTGCAGATTATTAATGGGATATTAT 1326
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QY 181 AATGAGCAATATGATAGCTGTCAGATGTTCTGAATAAAGTTCAGTGAAGAAAA 236
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 DB 1327 AATGAGCAATATGATAGCTGTCAGATGTTCTGAATAAAGTTCAGTGAAGAAAA 1382
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Search completed: March 17, 2003, 19:28:59
 Job time : 1220 secs

